

22910

STIC-Biotech/ChemLib

From: Mertz, Prema
Sent: Wednesday, August 16, 2000 9:07 AM
To: STIC-Biotech/ChemLib
Subject: 09/361,655

Please search SEQ ID NO: 12 with protein databases.

Thanks

Prema Mertz

Prema Mertz, Ph.D.
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Crystal Mall 1, Room 10E01
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U.S. Patent & Trademark Office

12

Edward Hart
Technical Info Specialist
STIC / Biotech
CM1 12C14 Tel: 305-9203



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the 1972
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Db 292 ASHSAVSVSLKANNPMPASTSCVPTARRPISLILDHNGNVKTVDPMVVEACGCS 350
 OY 61 ASHSAVSVSLKANNPMPASTSCVPTARRPISLILDHNGNVKTVDPMVVEACGCS 119

RESULT 2
 ID W60619 standard; Protein: 350 AA.
 AC W60619;
 DT 01-FEB-1999 (first entry)
 DE Human liver activin beta e polypeptide.
 KW Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
 KW erythroid; ovarian follicular maturation; hormone; neuronal survival;
 KW spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
 KW osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;
 KW menstrual disorder; transgenic; modulator; human.
 OS Homo sapiens.
 FH Key
 FT Peptide 1..17 Location/Qualifiers
 FT /note="signal sequence"
 FT Domain 18..236
 FT /note="propeptide domain"
 FT Modified_site 198..200
 FT /note="Asn is putatively N-glycosylated"
 FT Cleavage_site 232..236
 FT /note="endoproteolytic cleavage site"
 FT 237..350
 FT /note="mature growth factor domain"
 FT Domain
 FT W09822492-A1.
 FT 28-MAY-1998.
 FT 20-NOV-1997; US-752919.
 FT (DMM1) UNIV MICHIGAN.
 FT Bonadio J, Fang J;
 DR WPI: 98-312408/27.
 DR N-PSDB: V38240.
 PT New isolated nucleic acid encoding sub-units of liver activin -
 PT useful for regulating growth and differentiation of cells, e.g. for
 PT treating liver, bone and haematopoietic disorders
 PS Disclosure: Fig 5; 141pp; English.
 CC This represents a human liver activin beta e polypeptide. The invention
 CC provides murine beta c and beta e polypeptides and the encoding genes.
 CC Disorders of cell growth or differentiation (or susceptibility to them)
 CC are diagnosed by measuring liver activin gene activity or by detecting a
 CC mutation in the liver activin gene. Disorders of haematopoiesis,
 CC erythroid differentiation, ovarian follicular maturation, hormone
 CC secretion, neuronal survival, spermatogenesis, bone formation, insulin
 CC secretion or cardiac morphogenesis are some conditions that can be
 CC diagnosed using the liver activin. Cell growth and differentiation can be
 CC stimulated by treatment with an liver activin compound or agent that
 CC upregulates the compound's expression. Antagonists can be used to treat
 CC liver diseases while agonists can be used to increase growth and
 CC regeneration of liver tissue. The liver activin compound may also induce
 CC bone growth (e.g. for treating osteoporosis or osteomalacia) or
 CC haematopoiesis, particularly erythropoiesis, for treating haemophilia,
 CC cystic fibrosis or menstrual disorders. Antibodies (which bind to liver
 CC immunosassays, to generate anti-idiotypic antibodies (which bind to liver
 CC activin receptors) and to inhibit liver activin. Also, transgenic animals
 CC containing liver activin gene can be used to produce the liver activin
 CC (in correctly processed and modified forms) proteins, or the transgenic
 CC animals, are useful for screening for liver activin modulators.
 SQ Sequence 350 AA;

Query Match 99.7%; Score 913; DB 1; Length 350;
 Best Local Similarity 99.2%; Pred. No. 2,486-87;
 Matches 118; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 232 RARRPTCEPATPLCCRRDHYVDFELGWRDMLQPGGYOLNCSGCPPLHAGSPGIA 291
 OY 1 RARRPTCEPATPLCCRRDHYVDFELGWRDMLQPGGYOLNCSGCPPLHAGSPGIA 60
 Db 292 ASHSAVSVSLKANNPMPASTSCVPTARRPISLILDHNGNVKTVDPMVVEACGCS 350
 OY 61 ASHSAVSVSLKANNPMPASTSCVPTARRPISLILDHNGNVKTVDPMVVEACGCS 119

RESULT 3
 ID W60618 standard; Protein: 350 AA.
 AC W60618;
 DT 01-FEB-1999 (first entry)
 DE Murine liver activin beta e polypeptide.
 KW Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
 KW erythroid; ovarian follicular maturation; hormone; neuronal survival;
 KW spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
 KW osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;
 KW menstrual disorder; transgenic; modulator.
 OS Mus sp.
 FH Key
 FT Peptide 1..21 Location/Qualifiers
 FT /note="signal sequence"
 FT Domain 22..236
 FT /note="propeptide domain"
 FT Modified_site 198..200
 FT /note="Asn is putatively N-glycosylated"
 FT Cleavage_site 232..236
 FT /note="endoproteolytic cleavage site"
 FT 237..349
 FT /note="mature growth factor domain"
 FT Domain
 FT W09822492-A1.
 FT 28-MAY-1998.
 FT 20-NOV-1997; US-752919.
 FT (DMM1) UNIV MICHIGAN.
 FT Bonadio J, Fang J;
 DR WPI: 98-312408/27.
 DR N-PSDB: V38238.
 PT New isolated nucleic acid encoding sub-units of liver activin -
 PT useful for regulating growth and differentiation of cells, e.g. for
 PT treating liver, bone and haematopoietic disorders
 PS Claim 16; Fig 2; 141pp; English.
 CC This represents a murine liver activin beta e polypeptide. Sequences
 CC derived from a beta c cDNA clone is used for screening and cloning the
 CC activin beta e gene. Disorders of cell growth or differentiation (or
 CC susceptibility to them) are diagnosed by measuring liver activin gene
 CC activity or by detecting a mutation in the liver activin gene. Disorders
 CC of haematopoiesis, erythroid differentiation, ovarian follicular
 CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone
 CC formation, insulin secretion or cardiac morphogenesis are some conditions
 CC that can be diagnosed using the liver activin. Cell growth and
 CC differentiation can be stimulated by treatment with an liver activin
 CC compound or agent that upregulates the compound's expression. Antagonists
 CC can be used to treat liver diseases while agonists can be used to
 CC increase growth and regeneration of liver tissue. The liver activin
 CC compound may also induce bone growth (e.g. for treating osteoporosis or
 CC osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for
 CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies
 CC are useful in immunosassays, to generate anti-idiotypic antibodies (which
 CC bind to liver activin receptors) and to inhibit liver activin. Also,
 CC transgenic animals containing liver activin gene can be used to produce
 CC the liver activin (in correctly processed and modified forms) proteins,
 CC or the transgenic animals, are useful for screening for liver activin
 CC modulators.
 SQ Sequence 350 AA;

Query Match 98.9%; Score 906; DB 1; Length 350;
 Best Local Similarity 97.5%; Pred. No. 1,496-86;
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 232 RARRPTCEPATPLCCRRDHYVDFELGWRDMLQPGGYOLNCSGCPPLHAGSPGIA 291
 OY 1 RARRPTCEPATPLCCRRDHYVDFELGWRDMLQPGGYOLNCSGCPPLHAGSPGIA 60
 Db 292 ASHSAVSVSLKANNPMPASTSCVPTARRPISLILDHNGNVKTVDPMVVEACGCS 350
 OY 61 ASHSAVSVSLKANNPMPASTSCVPTARRPISLILDHNGNVKTVDPMVVEACGCS 119

[illegible]

Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps

RESULT 9
ID P70203 standard: protein:

AC P70203;
 DT 09-APR-1991 (first entry)
 DE Sequence of human inhibin beta-chain precursor beta-A.
 KW Fertility control; contraception; hormone; spermatogenesis.
 OS Homo sapiens.
 PH Key
 FT modified_site location/Qualifiers
 FT 165..167
 FT /note="potential N-linked glycosylation sites"
 FT region 1..28
 FT /note="signal sequence"
 FT region 28..310
 FT /note="pro region"
 FT protein 311..326
 FT cleavage_site 306..310
 FT /note="proteolytic processing site"
 PN EP-222491-A.
 DR 20-MAY-1987.
 PR 03-OCT-1986; 307586.
 PR 03-OCT-1985; US-783910.
 PR 10-FEB-1986; US-827710.
 PR 12-SEP-1986; US-906729.
 PA (GETH) GENENTECH INC.
 PI Mason AJ, Seeburg PH.
 WP: 87-137512/20.
 DR N-PSDB; N70315.
 PT Recombinant human or porcine inhibin or activin - used for
 PT modulating clinical condition or reproductive physiology of
 PT animals.
 PS Disclosure: Fig 8A; 48pp; English.
 CC A compsn. comprising human or porcine inhibin which is completely
 CC free of unidentified or porcine proteins is claimed. Also claimed
 CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
 CC chain. Sequencing of inhibin-encoding cDNA has led to the
 CC identification of prodomain regions located N-terminal to the
 CC mature inhibin chains that represent coordinately expressed
 CC biologically active polypeptides. The prodomain regions or
 CC prodomain immunogens are useful in monitoring preproinhibin
 CC processing in transformant cell culture or in experiments directed
 CC at modulating the clinical cond. or reproductive physiology of
 CC animals.
 SQ Sequence 426 AA:
 Query Match 54.4%; Score 498; DB 1; Length 426;
 Best Local Similarity 45.5%; Pred. No. 1,54e-41;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 306 RRRRGLECDGKVNICKKQPFVSKDIGNMDWIAPSGYHANYCEGCPSHIAGTSGSS 365
 QY 1 RARRPTCEPATPLCCRRDHYDFQELGWRDWTLOPEGYQLNVCSCPPHLAGSPGIA 60
 Db 366 LSFHSTVINHYRMGHSFPANLSCCVPTRKLRPMSTLYDDGQNIKKDIONMIVECCG 425
 QY 61 ASHSAVFS-L-LKANPMPASTSCCPTARRPLSLILDHNGNVKTDVPMVVEACGC 118
 Db 426 S 426
 QY 119 S 119
 RESULT 10
 ID R05413 standard; protein; 426 AA.
 AC R05413;
 DT 27-JUL-1990 (first entry)
 DE BUF-3 human differentiation inducing factor gene product.
 KW BUF-3; dhfr; dihydrofolic acid reductase; differentiation.
 OS Homo sapiens.
 PN J02009388-A.
 PD 12-JAN-1990.
 PR 8-JUL-1988; 170147.
 PR 9-MAR-1988; JP-055270.
 PA (ATIN) Ajinomoto KK.
 WP: 90-055348/08.
 DR N-PSDB; Q01648.

PT Physiologically active protein prepn. -
 PT by transforming plasmid having gene coding physiologically
 PT active protein and gene of dihydrofolic acid reductase to hamster
 PT ovary etc.
 PS Example 1; Fig 1; 12pp; Japanese.
 CC Gene may be expressed by transforming a dhfr negative strain of CHO cells
 CC with an active BUF-3 gene and dhfr carrying vector. BUF-3 gene product
 CC is a cell differentiating factor.
 SQ Sequence 426 AA;
 Query Match 54.4%; Score 498; DB 1; Length 426;
 Best Local Similarity 45.5%; Pred. No. 1,54e-41;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 306 RRRRGLECDGKVNICKKQPFVSKDIGNMDWIAPSGYHANYCEGCPSHIAGTSGSS 365
 QY 1 RARRPTCEPATPLCCRRDHYDFQELGWRDWTLOPEGYQLNVCSCPPHLAGSPGIA 60
 Db 366 LSFHSTVINHYRMGHSFPANLSCCVPTRKLRPMSTLYDDGQNIKKDIONMIVECCG 425
 QY 61 ASHSAVFS-L-LKANPMPASTSCCPTARRPLSLILDHNGNVKTDVPMVVEACGC 118
 Db 426 S 426
 QY 119 S 119
 RESULT 11
 ID P70200 standard; protein; 427 AA.
 AC P70200;
 DT 09-APR-1991 (first entry)
 DE Sequence of porcine inhibin beta-chain precursor beta-A.
 KW Fertility control; contraception; hormone; spermatogenesis.
 OS Sus scrofa domestica.
 PH Key
 FT region location/Qualifiers
 FT 1..308
 FT /note="used to design a long synthetic DNA probe"
 FT protein 309..424
 FT cleavage_site 304..308
 FT /note="proteolytic processing site"
 PN EP-222491-A.
 DR 20-MAY-1987.
 PR 02-OCT-1986; 307586.
 PR 03-OCT-1985; US-783910.
 PR 10-FEB-1986; US-827710.
 PR 12-SEP-1986; US-906729.
 PA (GETH) GENENTECH INC.
 PI Mason AJ, Seeburg PH.
 WP: 87-137512/20.
 DR N-PSDB; N70317.
 PT Recombinant human or porcine inhibin or activin - used for
 PT modulating clinical condition or reproductive physiology of
 PT animals.
 PS Disclosure: Fig 2B; 48pp; English.
 CC A compsn. comprising human or porcine inhibin which is completely
 CC free of unidentified or porcine proteins is claimed. Also claimed
 CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
 CC chain. Sequencing of inhibin-encoding cDNA has led to the
 CC identification of prodomain regions located N-terminal to the
 CC mature inhibin chains that represent coordinately expressed
 CC biologically active polypeptides. The prodomain regions or
 CC prodomain immunogens are useful in monitoring preproinhibin
 CC processing in transformant cell culture or in experiments directed
 CC at modulating the clinical cond. or reproductive physiology of
 CC animals.
 SQ Sequence 427 AA;
 Query Match 54.4%; Score 498; DB 1; Length 427;
 Best Local Similarity 45.5%; Pred. No. 1,54e-41;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 307 RRRRGLECDGKVNICKKQPFVSKDIGNMDWIAPSGYHANYCEGCPSHIAGTSGSS 366
 QY 1 RARRPTCEPATPLCCRRDHYDFQELGWRDWTLOPEGYQLNVCSCPPHLAGSPGIA 60

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RESULT	13
ID	R12088 standard; Protein; 116 AA.
AC	R12088;
DT	01-AUG-1991 (first entry)
DE	16.5 kD subunit of ovine inhibin.
KW	Follicle stimulating hormone; FSH; luteinizing hormone; LH; fertility; gonadotropin.
OS	Crambe abyssinica.
PN	U55015729-A.
PD	14-MAY-1991.
PE	23-JUN-1988; 210683.
PR	24-JUN-1986; US-678063.
PR	24-JUN-1988; US-210683.
PA	(SALK) SALK INST FOR BIOL STUD.
PI	Spies J, Rivier JEF, Bardin CW, Vale WW;
OR	WEL: 91-163615/22.

	Query Match	52.0%;	Score 476;	DB 1;	Length 116;	
	Best Local Similarity	45.18;	Pred. No. 3,76e-39;			
Matches	51;	Conservative	37;	Mismatches	28;	Indels 2; Gaps 2
Db	4 CDGKNICCKKEFFSEFKDIGNMDIIMPAGSYAHNCCGECECSHIAGSSGSLSPTSTYI	63				
Oy	9 CEPAPFLPCRDHRHVDFOGLGRWDIIQLPEXYOLNTSCGCCPHLAGSPGIASFSHFSAVF	68				
Db	64 NHYRRKRGISPFANLKSCVPTLRMSMLTYDOENLIIRKLDMNIYEBCGC	116				
Oy	69 S-L-TKANNPMPASTSCVPTRRPLSLTDIHNGVNATVDVDAVEACGCS	119				
RESULT	15					
ID	P80019 standard; Protein; 116 AA,					

Thu Aug 17 10:22:11 2000

US-08-765-662-12.rag

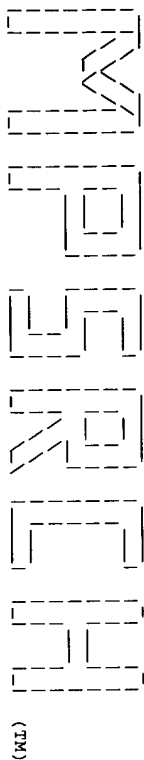
Page 7

CC P80019: (first entry)
 DT 28-JAN-1993
 DE Sequence of the 14k beta-chain of a protein exhibiting
 DE inhibin activity.
 KM Fertility control; inhibin; follicle stimulating hormone; inhibitor;
 KM gonadotropin.
 KW Homo. sapiens.
 PN US4737578-A.
 PN 12-APR-1988.
 PF 07-APR-1986; 848924.
 PF 10-FEB-1986; US-828435.
 PR 07-APR-1986; US-848924.
 PA (SALK) SALK INST FOR BIOL. STUD.
 PI Evans RM, Rosenfeld MG, Cerelli G, Mayo KE, Spleess J,
 PI Rivlier JEF, Valleeuw;
 DR WPI: 88-119128/17.
 CC New proteins with inhibin activity - esp. useful for controlling
 CC fertility in males
 CC Claim 1: Column 7-8; fpp; English.
 CC The inventors claim 2 proteins - A and B - each of which has a
 CC molecular weight of about 32k and is comprised of an alpha (18k) and
 CC a beta (14k) chain of human inhibin. The alpha chain is P80018.
 CC The beta chain is either P80019 or P80020. Proteins A and B are
 CC useful for regulating fertility of mammals. Each 32k protein
 CC exhibits inhibin activity in basal secretion of FHS but not
 CC inhibiting basal secretion of luteinizing hormone (LH).
 CC Sequence 116 AA.
 CC 50

	Query Match	Similarity	Score	DB	Length
Best Local	51.1%	45.1%	472	DB 1	116
Matches	51	Conservative	32	Mismatches	28
				Indels	2
				Gaps	2

	Query Match	Similarity	Score	DB	Length
Best Local	51.1%	45.1%	472	DB 1	116
Matches	51	Conservative	32	Mismatches	28
				Indels	2
				Gaps	2

Search completed: Thu Aug 17 10:15:45 2000
Job time : 24 secs.



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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Aug 17 10:16:03 2000; Maspar time 8.90 Seconds
Tabular output not generated. 630.799 Million cell updates/sec

Title: >US-08-765-662-12
Description: (1-119) from 5929213.pep
Perfect Score: 916
Sequence: 1 RARRPTCEPATPLCCRD.....NGNVKTDVPMVVEACGCS 119

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r64
1: p1r1 2: p1r2 3: p1r3 4: p1r4

Statistics: Mean 39.770; Variance 63.509; scale 0.626

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Alt No.	Score	Query Match	Length	ID	Description	Pred. No.
1	906	98.9	350	2	JC5241	8.86e-200
2	632	69.0	352	2	S70580	5.41e-129
3	629	68.7	352	2	JC5366	3.16e-128
4	619	67.6	367	2	JC54151	1.13e-125
5	616	67.2	352	2	JC52466	6.59e-125
6	503	54.9	425	2	I47072	2.83e-96
7	498	54.4	424	1	WEPGBA	5.11e-95
8	498	54.4	425	1	S31440	5.11e-95
9	498	54.4	425	1	S50898	5.11e-95
10	498	54.4	426	1	B42428	5.11e-95
11	487	53.2	424	1	B40905	2.95e-92
12	474	51.7	370	2	I51199	5.30e-89
13	472	51.5	413	2	JC4862	1.68e-88
14	471	51.4	255	2	I48235	2.98e-88
15	471	51.4	411	2	B41398	2.98e-88
16	468	51.1	349	1	WEPGBB	1.68e-87
17	468	51.1	407	1	A40150	1.68e-87
18	468	51.1	408	2	S50899	1.67e-86
19	464	50.7	393	2	I50103	3.06e-81
20	442	48.3	115	2	PN0506	8.97e-81
21	441	48.1	115	2	PN0505	1.57e-79
22	436	47.6	115	2	PN0504	4.00e-71
23	402	43.9	102	2	A36192	

24	388	42.4	101	2	C36192	inhibin beta-B2 chain	1.10e-67
25	386	42.1	101	2	B36192	inhibin beta-B1 chain	3.42e-67
26	355	38.8	398	2	JH0688	bone morphogenetic pr	1.26e-59
27	355	38.8	398	2	JH0687	bone morphogenetic pr	1.26e-59
28	352	38.4	400	2	A49147	bone morphogenetic pr	6.72e-59
29	352	38.4	401	2	JH0689	bone morphogenetic pr	6.72e-59
30	352	38.4	408	2	S58791	bone morphogenetic pr	6.72e-59
31	352	38.4	408	2	S38343	bone morphogenetic pr	6.72e-59
32	352	38.4	408	1	BMH04	bone morphogenetic pr	6.72e-59
33	352	38.4	420	2	I49541	bone morphogenetic pr	1.7e-58
34	351	38.3	405	2	I50608	bone morphogenetic pr	2.05e-58
35	350	38.2	393	2	S37073	bone morphogenetic pr	2.05e-58
36	350	38.2	394	2	S45355	bone morphogenetic pr	2.05e-58
37	350	38.2	396	1	BMH02	bone morphogenetic pr	1.91e-57
38	346	37.8	353	2	I50607	bone morphogenetic pr	3.10e-56
39	341	37.2	372	2	C39364	bone morphogenetic pr	9.42e-56
40	339	37.0	408	2	JH0801	bone morphogenetic pr	2.64e-54
41	333	36.4	373	2	PN0042	activin - fruit fly (8.00e-54
42	331	36.1	360	2	A29619	Vg1 embryonic growth	8.00e-54
43	331	36.1	513	1	BMH06	bone morphogenetic pr	7.34e-53
44	327	35.7	207	2	S37618	vgr protein - rat (fr	7.34e-53
45	327	35.7	510	2	A54798	vgr-I-related protein	7.34e-53

ALIGNMENTS

RESULT 1
ENTRY JC5241 #type complete
TITLE activin beta E chain precursor - mouse
ORGANISM Mus musculus #common_name house mouse
DATE 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 26-Aug-1999

ACCESSIONS JC5241; JC5367
REFERENCE JC5241
#authors Fang, J.; Yin, W.; Smiley, E.; Wang, S.Q.; Bonadio, J.
#journal Biochem. Biophys. Res. Commun. (1996) 228:669-674
#title Molecular cloning of the mouse activin beta E subunit gene.
#cross-references MIM:97096313
#contents liver
#accession JC5241

#molecule_type mRNA
#residues 1-350 #label FAN
#cross-references GB:096386; NID:g2072521; PID:g2072522

REFERENCE JC5366
#authors Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.
#journal Biochem. Biophys. Res. Commun. (1997) 231:655-661
#title Genes coding for mouse activin beta C and beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues.
#cross-references MIM:97224404

#accession JC5367
#molecule_type DNA
#residues 1-350 #label FA2
#cross-references GB:096386; NID:g2072521; PID:g2072522
COMMENT This protein is a member of the transforming growth factor-beta superfamily. There are three activins, A, B, and AB consisting of different combination of beta subunits.
COMMENT Activin beta C and beta E form a distinct subset of related activins.

GENETICS 99/3
CLASSIFICATION #superfamily inhibin
SUMMARY #length 350 #molecular-weight 39057 #checksum 2625

Query Match 98.9%; Score 906; DB 2; Length 350;
Best Local Similarity 97.3%; Pred. No. 8.86e-200;
Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db	232	RARRPTCEPATPLCCRDHYVDFELGMDWIQPEGYQINTSGGCPHLAGSGIA	291
QY	1	RARRPTCEPATPLCCRDHYVDFELGMDWIQPEGYQINTSGGCPHLAGSGIA	60
Db	292	ASFRSAVFSILKANPNWPAAGSCVPTARRPPLSLYLDHNGNVKTDVDMVVEACGCS	350

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QY      61  ASFHSAVFSLTKANNMPPASTSCCVPTARRPRLSLTYLDHNGVNVKTDVPMVEARGCGS  119
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ENTRY   2
TITLE   activin beta C precursor - mouse
ORGANISM
#authors
#journal
#title
#cross-references MUID:96283807
#accession
#status
#molecule_type DNA
##residues 1-352 ##label LAU
##cross-references EMBL:040772
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#introns
CLASSIFICATION
SUMMARY #superfamily inhibin
#length 352 #molecular-weight 39401 #checksum 5176

Query Match 69.0%; Score 632; DB 2; Length 352;
Best Local Similarity 63.6%; Pred. No. 5,416-129;
Matches 77; Conservative 26; Mismatches 16; Indels 2; Gaps 2

Db      232  RYRRRGIDCGASRMCCROEPFYDREIGWMDITIQPEGYAMNCTGQCPPLHVAAGMFCIS  291
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QY      1  RARRRPTCEPRLPCCRRDHYDVELGWRWILQPEGYOLNCSGQCPPLHAGSPGIA  60
|||||
Db      292  ASFHTAVNLKANAAGTTGSGCCVPTSRRLSLTYLRDSNIVXTDIDPMVEARGCG  351
|||||
QY      61  ASFHSAVFSLTKANNPM-PAS-TSCCVPPTARRPRLSLTYLDHNGVNVKTDVPMVEARGCG  118
|||||
Db      352  S 352
QY      119  S 119

RESULT  3
ENTRY   3
TITLE   activin beta C - mouse
ORGANISM
#formal_name Mus musculus #common_name house mouse
DATE    28-May-1997 #sequence_revision 18-Jul-1997 #text_change
26-Aug-1999
#cross-references MUID:97224404
#accession
#molecule_type DNA
##residues 1-352 ##label FAN
##cross-references GB:U091962
COMMENT Activin beta C and beta E form a distinct subset of related
activins.
GENOTYPE
#introns
CLASSIFICATION
SUMMARY #superfamily inhibin
#length 352 #molecular-weight 39387 #checksum 5266

Query Match 68.7%; Score 629; DB 2; Length 352;
Best Local Similarity 62.8%; Pred. No. 3,156-128;
Matches 76; Conservative 27; Mismatches 16; Indels 2; Gaps 2;

Db      232  RYRRRGIDCGASRMCCROEPFYDREIGWMDITIQPEGYAMNCTGQCPPLHVAAGMFCIS  291

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Qy	1	RARRRTTGPCEAPPLCCRRDHYDVEQELGMRDWIIQEPGLOLNTCSQCCPPHLAGSPGIA	60
Db	292	ASFTAVLNLKNNAAAGTTGRSCCPTSRRLPSLYRDSNIVYTDLPDMVYACGC	351
Qy	61	ASFSAVFSILKANNPW-PAS-TSCCVPTARRPISLYLTDHNGNVYKTDVPDMVYACGC	118
Db	352	S	352
Qy	119	S	119
RESULT	4		
ENTRY	JC4151	#type complete	
TITLE	activin beta d chain precursor - African clawed frog		
ORGANISM	#formal_name Xenopus laevis #common_name African clawed frog		
DATE	27-Aug-1993 #sequence_revision 19-Oct-1993 #text_change 26-Aug-1999		
ACCESSIONS	JC4151		
REFERENCE	JC4151		
#authors	Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.		
#journal	Biochem. Biophys. Res. Commun. (1993) 210:581-588		
#title	Molecular cloning and functional analysis of a new activin beta subunit: a dorsal mesoderm-inducing activity in Xenopus.		
#cross-references	MUID:95275314		
#accession	JC4151		
#molecule_type	mRNA		
##residues	1-367	#label ODA	
##cross-references	DDbT:D995f3; NID:g961512; PID:d1009105; PID:g961513		
##experimental_source	embryo		
CLASSIFICATION	#superfamily inhibin		
KEYWORDS	glycoprotein; mesoderm		
FEATURE			
1-253			
254-367			
64,155,161,208,			
230			
SUMMARY			
	#binding_site carbohydrate (Asn) (covalent) #status predicted		
	#length 367 #molecular_weight 41729 #checksum 2774		
	Query Match		
	Best Local Similarity 67.6%; Score 619; DB 2; Length 367;		
	Matches 74; Conservative 25; Mismatches 20; Indels 0; Gaps 0;		
Db	249	HATKSLNCDONSNLCCRRDYVDFKIDGNMDWIIKPEGYQIYMGGLCPMHIAAPGMA	308
Qy	1	RARRRTTGPCEAPPLCCRRDHYDVEQELGMRDWIIQEPGLOLNTCSQCCPPHLAGSPGIA	60
Db	309	ASFTAVLNLKANNIQTAVNSCCVPPKRRPPLSMILFDKRNANNVLTDTADMTVEACGCS	367
Qy	61	ASFSAVFSILKANNPWPASTSCCVPTARRPISLYLTDHNGNVYKTDVPDMVYACGCS	119
RESULT	5		
ENTRY	JC2466	#type complete	
TITLE	inhibin beta C-chain precursor - human		
ALTERNATE_NAMES	activin beta C chain		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	29-Mar-1993 #sequence_revision 26-May-1993 #text_change 26-Aug-1999		
ACCESSIONS	JC2466		
REFERENCE	JC2466		
#authors	Hoetten, G.; Neidhardt, H.; Schneider, C.; Pohl, J.		
#journal	Biochem. Biophys. Res. Commun. (1993) 206:608-613		
#title	Cloning of a new member of the TGF-beta family: A putative new activin beta C chain.		
#cross-references	MUID:95126961		
#accession	JC2466		
#molecule_type	mRNA		
##residues	1-352	#label HOE	
#cross-references	GB:X82340; NID:g669154; PIDN:CAA57890.1; PID:g669155		

```

##experimental source liver
COMMENT      This protein is a member of the TGF-beta superfamily, activins
              compose of homo or heterodimers of the beta A and beta B chain.
GENETICS
#gene        GDB:INHBC
#cross-references GDB:632884
#map_position 2cen-2q13
CLASSIFICATION #superfamily inhibin
KEYWORDS      glycoprotein
FEATURE
1-18          #domain signal sequence #status predicted #label SIG\
19-236        #domain propeptide #status predicted #label PRO\
237-352       #product activin beta C #status predicted #label MAT\
110,143,161   #binding_site carbohydrate (asn) (covalent) #status
              predicted
SUMMARY       #length 352 #molecular-weight 38238 #checksum 8314

Query Match 67.2%; Score 616; DB 2; Length 352;
Best Local Similarity 63.9%; Pred. No. 6,59e-125;
Matches 76; Conservative 26; Mismatches 15; Indels 2; Gaps 2;

Db 234 HRRGIDCGSGMCCRGFEFVFRHGHWDHIOPEGYAMFCIGCCPLHAGMPGIAAS 293
QY 3 RRRPTCEPATPLCCRRDHYVDFDELGWRDWILOPEGYQLVCSGQCPHLAGSPGIAAS 62
DB 294 FHTAVLNLKATTAAGTTGGGSCVPTARRPLSLHYDRDSNIVYTDIPDMVAVACGCS 352
QY 63 FHSAYVSLKANNPW-PAST-SCVPTARRPLSLYLDHNGVAVTDPDMVAVACGCS 119

RESULT 6
ENTRY      147072 #type complete
TITLE      Inhibin beta-A chain precursor - sheep
ORGANISM   #formal_name Ovis orientalis aries, Ovis ammon aries
            #common_name domestic sheep
DATE       15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change
            15-Jul-1999
ACCESSIONS 147072
REFERENCE  147072
#authors   Fleming, J.S.; Gallowsay, S.M.; Crawford, R.J.; Tisdall, D.J.;
            Greenwood, P.J.
#journal   Mol. Reprod. Dev. (1995) 40:1-8
#title     Tissue-specific variation in the length of the 5'
            untranslated region of the beta A-inhibin mRNA in sheep.
#cross-references M01D:95217464
#accession 147072
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-425 #label FLE
#cross-references GB:L19218; NID:g310379; PIDN:AA041621.1; PID:g310380
REFERENCE  A60856
#authors   Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.;
            Hearn, M.T.W.; Wettenthal, R.E.H.; Findlay, J.K.; Burger,
            H.G.; de Kretser, D.M.
#journal   J. Endocrinol. (1987) 113:213-221
#title     Isolation of inhibin from ovine follicular fluid.
#cross-references M01D:87224684
#accession B60856
#molecule_type protein
#residues  310-312, 'X', 314-319, 'XX', 322 #label LEV
COMMENT     Inhibin suppresses follicle-stimulating hormone secretion.
KEYWORDS    disulfide bond; glycoprotein; gonad; heterodimer; hormone
SUMMARY     #length 425 #molecular-weight 47565 #checksum 2083

Query Match 54.9%; Score 503; DB 2; Length 425;
Best Local Similarity 46.3%; Pred. No. 2,83e-96;
Matches 56; Conservative 31; Mismatches 32; Indels 2; Gaps 2;

Db 305 RRRRGLEDGKVNICKCKQFYVFKDIGNWMIAPSGYHANYCEGCPSHIAGTSGSS 364
QY 1 RARRRPTCEPATPLCCRRDHYVDFDELGWRDWILOPEGYQLVCSGQCPHLAGSPGIA 60


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Db 365 LSFHSTVINHYRMCHSPFANLKSCVPTKLRPMSTMITYDDGQNIKKDQNNIVECCG 424
QY 61 ASFHSAVFS-L-LKANNPWPASTSCVPTARRPLSLYLDHNGVAVTDPDMVAVACG 118
Db 425 S 425
QY 119 S 119

RESULT 7
ENTRY      WEPGBA #type complete
TITLE      Inhibin beta-A chain precursor - pig
ORGANISM   #formal_name Sus scrofa domestica #common_name domestic pig
DATE       13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change
            18-Jun-1999
ACCESSIONS A01393
REFERENCE  A93371
#authors   Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.;
            Ying, S.Y.; Guillemin, R.; Miall, H.; Seeburg, P.H.
#journal   Nature (1985) 318:659-663
#title     Complementary DNA sequences of ovarian follicular fluid
            inhibin show precursor structure and homology with
            transforming growth factor-beta.
#cross-references M01D:86092207
#accession A01393
#molecule_type mRNA
#residues  1-424 #label MAS
#cross-references GB:X03266; NID:g2002; PIDN:CA27020.1; PID:g2003
COMMENT     The source of this protein is ovarian follicular fluid.
            The mature protein is the carboxyl-terminal segment of a precursor
            polypeptide; the active molecule is a dimer of one beta and one
            alpha chain, linked by one or more disulfide bonds. Two different
            forms of inhibin have been isolated (A and B) that differ in the
            amino-terminal sequence of their beta chains.
            Inhibin is secreted by ovaries or testes and inhibits the secretion
            of follicleotropin by the pituitary gland.
            #superfamily inhibin
            #follicleotropin inhibitor; glycoprotein; gonad
            #contraceptive; follicleotropin inhibitor; glycoprotein; gonad
            #predicted
            #binding_site carbohydrate (asn) (covalent) #status
            predicted
SUMMARY     #length 424 #molecular-weight 47476 #checksum 1246

Query Match 54.4%; Score 498; DB 1; Length 424;
Best Local Similarity 45.5%; Pred. No. 5,11e-95;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 304 RRRRGLEDGKVNICKCKQFYVFKDIGNWMIAPSGYHANYCEGCPSHIAGTSGSS 363
QY 1 RARRRPTCEPATPLCCRRDHYVDFDELGWRDWILOPEGYQLVCSGQCPHLAGSPGIA 60
Db 364 LSFHSTVINHYRMCHSPFANLKSCVPTKLRPMSTMITYDDGQNIKKDQNNIVECCG 423
QY 61 ASFHSAVFS-L-LKANNPWPASTSCVPTARRPLSLYLDHNGVAVTDPDMVAVACG 118

RESULT 8
ENTRY      S31440 #type complete
TITLE      Inhibin beta-A chain - mouse
ALTERNATE_NAMES  inhibin A; mesoderm-inducing factor WEHI-MIF
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
            10-Sep-1999
ACCESSIONS A60087; I48265; S31440
REFERENCE  A60087


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<p>#authors Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nijmen, K.; Isaacs, H.V.; Slack, J.M.W.; Smith, J.C.</p> <p>#journal Development (1990) 110:435-443</p> <p>#title A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia cells is activin A.</p> <p>#cross-references MIM:9215098</p> <p>#accession A60087</p> <p>#molecule_type protein</p> <p>#residues 309-311, 'X', 313-318, 'XX', 321-325 #label AL2</p> <p>REFERENCE</p> <p>#authors Albano, R.M.; Groome, N.; Smith, J.C.</p> <p>#journal Development (1993) 117:711-723</p> <p>#title Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.</p> <p>#cross-references MIM:93321614</p> <p>#accession I48265</p> <p>#status preliminary; translated from GB/EMBL/DBJ</p> <p>#molecule_type mRNA</p> <p>#residues 1-424 #label RES</p> <p>#cross-references EMBL:X69619; NID:950145; PIDN:CAA9325.1; FID:950146</p> <p>IRFICATION #superfamily inhibin</p> <p>SUMMARY #length 424 #molecular-weight 47392 #checksum 2136</p> <p>Query Match 54.4%; Score 498; DB 1; Length 424; Best Local Similarity 45.5%; Pred. No. 5.11e-95; Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;</p> <p>Db 304 RRRRGLEDCGKVNICKKPFVDFKIDGNDWITLPSGYHANCCEGCPHSIAGTSGS 363 : : : : : : 1 RARRRTPICEAPPLCCRDHYDFQELGWRMDLPEGYVNLGCGCPHLAGSPGIA 60 : : : : : : 364 LSFHSTVINHRMGHSFPAFLKSCCVPTLRPSMLYYDDGNIITKRIQMWIYEGGC 423 : : : : : : 61 ASFHSAYFS-L-LKANPWPASTSCCVPTARRPLSLTYLDHNGNVKTDVPMVVEACGC 118</p> <p>Db 424 S 424 QY 119 S 119</p> <p>RESULT 9</p> <p>ENTRY S50898 #type complete</p> <p>TITLE Inhibin beta-A chain precursor - bovine</p> <p>ALTERNATE_NAMES activin; mesoderm inducing factor</p> <p>ORGANISM #formal_name Bos primigenius taurus #common_name cattle</p> <p>DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999</p> <p>ACCESSIONS S50898; B25732; A60960; B61548</p> <p>SEQUENCE S50897</p> <p>#authors Thompson, D.A.; Cronin, C.N.; Martin, F.</p> <p>#journal Eur. J. Biochem. (1994) 226:751-764</p> <p>#title Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B)-inhibin/activin genes. Identification of transcription factor AP-2-binding sites in the 5'-flanking regions by DNase I footprinting.</p> <p>#cross-references MIM:95112839</p> <p>#accession S50898</p> <p>#status preliminary</p> <p>#molecule_type DNA</p> <p>#residues 1-425 #label THO</p> <p>#cross-references EMBL:U16238</p> <p>REFERENCE A94097</p> <p>#authors Forage, R.G.; Ring, J.M.; Brown, R.W.; McInerney, B.V.; Cobon, G.S.; Gregson, R.P.; Robertson, D.M.; Morgan, F.J.; Heatr, M.T.W.; Findlay, J.K.; Wettenthal, R.E.H.; Burger, H.G.; De Kretser, D.M.</p> <p>#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3091-3095</p> <p>#title Cloning and sequence analysis of cDNA species coding for the two subunits of inhibin from bovine follicular fluid.</p> <p>#cross-references MIM:86205842</p> <p>#accession B25732</p> <p>#molecule_type mRNA</p>	<p>#residues 258-425 #label FOR</p> <p>#cross-references GB:M13272; NID:9163196; PIDN:AA97415.1; PID:9163197</p> <p>#note part of this sequence, including the amino end of the mature protein, was confirmed by protein sequencing</p> <p>REFERENCE</p> <p>#authors Chertov, O.Y.; Krasnosel'ski, A.L.; Bogdanov, M.E.; Hoperskaya, O.A.</p> <p>#journal Biomed. Sci. (1990) 1:499-506</p> <p>#title Mesoderm-inducing factor from bovine amniotic fluid: purification and N-terminal amino acid sequence determination</p> <p>#cross-references MIM:92126853</p> <p>#accession A60960</p> <p>#molecule_type protein</p> <p>#residues 310-312, 'X', 314-319, 'XX', 322-328, 'P' #label CHE</p> <p>REFERENCE</p> <p>#authors Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, K.; Matsuo, H.</p> <p>#journal Mol. Cell. Endocrinol. (1986) 44:55-60</p> <p>#title Isolation of bovine follicular fluid inhibin of about 32 kDa</p> <p>#cross-references MIM:86133989</p> <p>#accession B61548</p> <p>#molecule_type protein</p> <p>#residues 310-313 #label FUK</p> <p>GENETICS #introns 130/1</p> <p>CLASSIFICATION #superfamily inhibin</p> <p>KEYWORDS disulfide bond; glycoprotein; gonad; heterodimer; homodimer; hormone</p> <p>FEATURE</p> <p>1-28 #domain signal sequence #status predicted #label SIG\</p> <p>29-309 #domain propeptide #status predicted #label PRO\</p> <p>310-425 #product beta-A inhibin/activin #status experimental #label MAY\</p> <p>165 #binding_site carboxydrate (Asn) (covalent) #status predicted</p> <p>SUMMARY #length 425 #molecular-weight 47521 #checksum 898</p> <p>Query Match 54.4%; Score 498; DB 1; Length 425; Best Local Similarity 45.5%; Pred. No. 5.11e-95; Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;</p> <p>Db 305 RRRRGLEDCGKVNICKKPFVDFKIDGNDWITLPSGYHANCCEGCPHSIAGTSGS 364 : : : : : : 1 RARRRTPICEAPPLCCRDHYDFQELGWRMDLPEGYVNLGCGCPHLAGSPGIA 60 : : : : : : 365 LSFHSTVINHRMGHSFPAFLKSCCVPTLRPSMLYYDDGNIITKRIQMWIYEGGC 424 : : : : : : 61 ASFHSAYFS-L-LKANPWPASTSCCVPTARRPLSLTYLDHNGNVKTDVPMVVEACGC 118</p> <p>Db 425 S 425 QY 119 S 119</p> <p>RESULT 10</p> <p>ENTRY B24248 #type complete</p> <p>TITLE Inhibin beta-A chain precursor - human</p> <p>ALTERNATE_NAMES activin A; activin AB chain A; erythroid differentiation factor; megakaryocyte differentiation active protein</p> <p>ORGANISM #formal_name Homo sapiens #common_name man</p> <p>DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999</p> <p>ACCESSIONS S30488; B23556; B24248; A30884; S33531; PNM010</p> <p>SEQUENCE S30488</p> <p>#authors Tanimoto, K.; Handa, S.I.; Deno, N.; Murakami, K.; Fukamizu, A.</p> <p>#journal DNA Seq. (1991) 2:103-110</p> <p>#title Structure and sequence analysis of the human activin beta(A) subunit gene.</p> <p>#cross-references MIM:92135888</p> <p>#accession S30488</p> <p>#status preliminary</p>
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##molecule-type DNA
##residues 1-426 ##label TAN
##cross-references EMBL:X57578; NID:g28351; PIDN:CAA0805.1; PID:g825621
##note the authors translated the codon GAG for residue 53 as
Gly and GAG for residue 56 as Gly
REFERENCE
#authors A91366
#journal Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.;
#journal Forde, R.G.
#journal FEBS Lett. (1986) 206:328-334
#title Human inhibin genes. Genomic characterisation and sequencing.
#cross-references NID:87005283
#accession B2356
##molecule-type DNA
##residues 311-426 ##label STE
##cross-references GB:X04447; NID:g33928; PIDN:CAA2804.1; PID:g33929
REFERENCE
#authors A90123
#journal Mason, A.J.; Niall, H.D.; Seeburg, P.H.
#journal Blochem. Biophys. Res. Commun. (1986) 135:957-964
#title Structure of two human ovarian inhibins.
#cross-references NID:86186863
#accession B24248
##molecule-type mRNA
##residues 1-426 ##label MAS
##cross-references GB:M13436; NID:g186414; PIDN:AA59168.1; PID:g307069
REFERENCE
#authors A30884
#journal Murata, M.; Eto, Y.; Shibai, H.; Sakai, M.; Muramatsu, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1988) 85:2434-2438
#title Erythroid differentiation factor is encoded by the same mRNA
as that of the inhibin beta-A chain.
#cross-references NID:88190086
#accession A30884
##molecule-type mRNA
##residues 1-426 ##label MUR
##cross-references GB:J03634; NID:g181946; PIDN:AA435787.1; PID:g181947
REFERENCE
#authors S33351
#journal Berg, H.; Walter, M.; Northemann, W.
#journal Submitted to the EMBL Data Library, April 1993
#title Nucleotide sequence coding for the mature subunit beta(A) of
human inhibin in testis.
#accession S33351
##status preliminary
##molecule-type mRNA
##residues 311-376, 'AC', 380-426 ##label BER
##cross-references EMBL:X72498; NID:g297786; PIDN:CAA51163.1;
PID:g755740
REFERENCE
#authors PND010
#journal Fujimoto, K.; Kawakita, M.; Kato, K.; Yonemura, Y.; Masuda,
#journal T.; Matsuzaki, H.; Hirose, J.; Isaji, M.; Sasaki, H.;
#journal Inoue, T.; Takatsuki, K.
#journal Biochem. Biophys. Res. Commun. (1991) 174:1163-1168
#title Purification of megakaryocyte differentiation activity from a
human fibrous histiocyte cell line: N-terminal sequence
homology with activin A.
#cross-references NID:91144591
#accession PND010
##molecule-type protein
##residues 311-313, 'X', 315-320, 'XX', 323-328, 'X', 330-334 ##label FUJ
#comment Activins A and B are homodimers of inhibin beta-A or inhibin
beta-B, respectively, while activin AB is a heterodimer. Inhibins
A and B are heterodimers of the inhibin alpha chain with inhibin
beta-A and beta-B, respectively.
GENETICS
#genes GDB:INHBA
#cross-references GDB:119346; OMIM:147290
#map_position 7p15-7p13
#introns 129/3
#superfamily inhibin
#glycoprotein; gonad; heterodimer; homodimer; hormone
CLASSIFICATION
#domain signal sequence #status predicted #label SIG\
1-28 #domain propeptide #status predicted #label PRO\
29-310 #product inhibin beta A chain #status experimental
311-426 #label MAT\

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165 #binding site carbohydrate (Asn) (covalent) #status
SUMMARY #length 426 #molecular-weight 47442 #checksum 3853
Query Match 54.4%; Score 498; DB 1; Length 426;
Best Local Similarity 45.5%; Pred. No. 5,11e-95;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
Db 306 RRRRGLEDGKYNICCKKQFFVSFKDIGMNDWIAPSGYANACEGCPSHIAGTSGSS 365
1 RARRPTCEPATPLCCRDHYDFOELGMRDWILOPGYOLNCSQCPHLAAGSPGIA 60
Oy 366 LSFSTVINYHNRGHSPPANIKSCCVPTKLRPMSMTLYDDGNIIRKDIQNNIVECCG 425
61 ASFSHAFVS-L-LKANNPWPASTSCVPTARRPRLSLYLDMGNVVTVDVPMVVEACGC 118
Oy 426 S 426
119 S 119
RESULT 11
ENTRY B40905 #type complete
TITLE Inhibin beta-A chain precursor - rat
ORGANISM Rattus norvegicus #common_name Norway rat
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
10-Sep-1999
ACCESSIONS B40905; B40056
REFERENCE
#authors Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason,
#journal A.J.; Ying, S.Y.; Ueno, N.; Ling, N.
#journal Mol. Endocrinol. (1987) 1:388-396
#title Complementary deoxyribonucleic acid (cDNA) cloning and DNA
sequence analysis of rat ovarian inhibins.
#cross-references MGI:90331931
#accession B40905
##status preliminary; not compared with conceptual translation
##molecule-type mRNA
##residues 1-424 ##label ESC
REFERENCE
#authors A40056
#journal Woodruff, T.K.; Meunier, H.; Jones, P.B.C.; Hsueh, A.J.W.;
#journal Mayo, K.E.
#journal Mol. Endocrinol. (1987) 1:561-568
#title Rat inhibin: molecular cloning of alpha- and beta-subunit
complementary deoxyribonucleic acids and expression in the
ovary.
#cross-references NID:91042598
#accession B40056
##status preliminary
##molecule-type mRNA
##residues 1-366, 'H', 368-424 ##label WOO
##cross-references GB:X7482; NID:g204936; PIDN:AA44136.1; PID:g204937
CLASSIFICATION #superfamily inhibin
SUMMARY #length 424 #molecular-weight 47356 #checksum 1734
Query Match 53.2%; Score 487; DB 1; Length 424;
Best Local Similarity 44.6%; Pred. No. 2.95e-92;
Matches 54; Conservative 32; Mismatches 33; Indels 2; Gaps 2;
Db 304 RRRRGLEDGKYNICCKKQFFVSFKDIGMNDWIAPSGYANACEGCPSHIAGTSGSS 363
1 RARRPTCEPATPLCCRDHYDFOELGMRDWILOPGYOLNCSQCPHLAAGSPGIA 60
Oy 61 ASFSHAFVS-L-LKANNPWPASTSCVPTARRPRLSLYLDMGNVVTVDVPMVVEACGC 118
Oy 424 S 424
119 S 119
RESULT 12

```

ENTRY	IS1199	#type complete
TITLE	activin beta B subunit - African clawed frog	
ORGANISM	#formal_name Xenopus laevis #common_name African clawed frog	
DATE	13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999	
ACCESSIONS	IS1199	
REFERENCE	Dohlmann, C.E.; Hemmati-Brivanlou, A.; Thomson, G.H.; Fields A.; Woolf, T.M.; Melton, D.A. Dev. Biol. (1993) 157:474-483	
#authors	Expression of activin mRNA during early development in Xenopus laevis.	
#title	Expression of activin mRNA during early development in Xenopus laevis.	
#cross-references	MUID:93273083	
#accession	IS1199	
#status	Preliminary; translated from GB/EMBL/DBJ	
##molecule-type	MRNA	
##residues	1-370 #label DOH	
##cross-references	GB:S61773; NID:g9386027; PIDN:AA26863.1; PID:g9386028	
CLASSIFICATION	#superfamily inhibin	
SUMMARY	#length 370 #molecular-weight 41678 #checksum 6606	
##try Match	51.7%; Score 474; DB 2; Length 370;	
#local Similarity	48.3%; Pred. No.5,30e-89;	
Matches	58; Conservative 25; Mismatches 36; Indels 1; Gaps 1;	
Db	251 RIRKRGLEDGHTNCCRGQYIDPRLIGNMNDITAPACGYANCGSPYLAGVGS310	
Oy	1 RARRRPTCEPATPLCCRDHYDFOELGMRDMLDPEGYOLNCSGCCPHLAGSG310	
Db	311 SPSHTAVVNOYRMGINSCEIPTKLTSTSMILYFDEYNIYKRDVPMNIVDEC370	
Oy	61 ASFSHSAVSFLKANNPWPAST-SCCVPTARRPSTLTYLDHNGNVKTDVPMNVAEACGCS119	
RESULT	13	
ENTRY	JC4862	
TITLE	activin beta-A chain precursor - newt	
ORGANISM	#formal_name Cynops pyrrhogaster #common_name newt	
DATE	15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 16-Jul-1999	
ACCESSIONS	JC4862	
REFERENCE	Yamamoto, T.; Nakayama, Y.; Abe, S. Biochem. Biophys. Res. Commun. (1996) 224:451-456	
#authors	Expression of activin beta subunit genes in sertoli cells of newt testes.	
#title	Expression of activin beta subunit genes in sertoli cells of newt testes.	
#cross-references	MUID:96295508	
#accession	JC4862	
##molecule-type	MRNA	
##residues	1-413 #label YAM	
##cross-references	GB:U84516; NID:g1502288; PIDN:BA12693.1; PID:d1013374; PID:g1502289	
COMMENT	##experimental_source testes	
##experimental_source	testes	
regulation	This protein is secreted from Sertoli cells and plays a role in the regulation of newt spermatogenesis.	
FEATURE	regulation of newt spermatogenesis.	
CLASSIFICATION	#superfamily inhibin	
##domain	signal sequence #status predicted #label SIG\	
#domain	activin beta-A chain #status predicted #label	
SUMMARY	#length 413 #molecular-weight 46303 #checksum 5572	
Query Match	51.5%; Score 472; DB 2; Length 413;	
Best Local Similarity	43.0%; Pred. No.1,68e-88;	
Matches	52; Conservative 33; Mismatches 34; Indels 2; Gaps 1;	
Db	293 RRRRGLECGKXKSLCKKQFYSPKIDGSDMWIAPPGYTNANCGCPMYITGSG352	
Oy	1 RARRRPTCEPATPLCCRDHYDFOELGMRDMLDPEGYOLNCSGCCPHLAGSG310	
Db	353 PSFHAIVINQYRRRGSPSTYSKSCVPTKIRASMSLYDDQDNIIKKIDQNVVE342	
Oy	61T ASFSHSAVSFL-UKANNPWPASTSCCVPTARRPSTLTYLDHNGNVKTDVPMNVAEACGCS118	

```

Db      413 S 413
Oy      119 S 119

RESULT  14
ENTRY   I48235 #type fragment
TITLE   inhibit beta-B chain - mouse (fragment)
ALTERNATE_NAMES
ORGANISM Mus musculus #common_name house mouse
DATE    02-Jul-1996 #sequence_revision 01-Aug-1997 #text_change
        16-Jul-1999
ACCESSIONS
REFERENCE I48235
#authors Rivas, O.; Thurl, T.; Eramaa, M.; Salnio, K.; Hilden, K.;
#journal Saxen, L.; Gilbert, S.F.
#title Mech. Dev. (1995) 50:229-245
#cross-references MIMD:95344997
#accession I48235
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues 1-234 ##label RES
##cross-references EMBL:X83376; NID:g603571; PIDN:CAA58290.1;
PID:g603572

REFERENCE I48243
#authors Albano, R.M.; Groome, N.; Smith, J.C.
#journal Development (1993) 117:711-723
#title Activins are expressed in preimplantation mouse embryos and
in ES and EC cells and are regulated on their
differentiation.
#cross-references MIMD:93321614

#accession I48266
#status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 134, D', 135-255 ##label ALB
##cross-references EMBL:X66620; NID:g50147; PIDN:CAA49326.1; PID:g50148
CLASSIFICATION #superfamily inhibitn
SUMMARY #length 255 #checksum 6134

Query Match 51.4%; Score 471; DB 2; Length 255;
Best Local Similarity 48.3%; Pred. No.2.98e-84;
Matches 58; Conservative 27; Mismatches 34; Indels 1; Gaps 1;

Db      136 RIRRGLECDGRTSLCCRQGFIDFLICGMNDWIATPGYGCNYCGSPAYLAGVPCSA 195
       1-1-1 : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      1 RARRPTCTEAPATPLCCRRDHVDYDFELTGRMWDIILDPESYQLNTYCSCGCPHLAESPia 60
       ::::: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      196 SSFRTAVVNOVRMGGLPBGVNSCCIPFKLSMSMYFPDEYNIVKRPVPNNIVEGCCA 255
       ::::: : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      61 ASFSNVAFSLIKANNPPAST-SCCFPTRARPLSLIXLDHNMNVKTIDVPDMVAVACGS 119
       ::::: : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT  15
ENTRY   B41398 #type complete
TITLE   inhibit beta-B chain precursor - rat
ALTERNATE_NAMES inhibit/activin beta B-chain
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE    03-Apr-1992 #sequence_revision 01-Aug-1997 #text_change
        16-Jul-1999
ACCESSIONS B41398; I53288; CA0905
REFERENCE A41398
#authors Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
#journal Mol. Endocrinol. (1989) 3:1914-1925
#title Analysis of the 5'-flanking regions of rat inhibit alpha-
beta-B-subunit genes suggests two different regulatory
mechanisms.
#cross-references MIMD:90190649

#accession B41398
#status preliminary
#molecule_type DNA

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##residues      1-174 ##label FEN
##cross-references GB:M32755; GB:M32757; NID:g2049493; PIDN:AAA4138.1;
PID:g554460

REFERENCE
#authors      Dykema, J.C.; Mayo, K.E.
#journal      Endocrinology (1994) 135:702-711
#title        Two messenger ribonucleic acids encoding the common beta
              B-chain of inhibin and activin have distinct 5'-initiation
              sites and are differentially regulated in rat granulosa
              cells.
#cross-references MUID:94307180
#accession    153288
#status       Preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues     1-7 ##label RES
#cross-references GB:S72477; NID:g619268
A40905
#authors      Esch, F.S.; Shimsaki, S.; Cooksey, K.; Mercado, M.; Mason,
              A.J.; Ying, S.Y.; Ueno, N.; Ling, N.
#journal      Mol. Endocrinol. (1987) 1:388-396
#title        Complementary deoxyribonucleic acid (cDNA) cloning and DNA
              sequence analysis of rat ovarian inhibins.
#cross-references MUID:90331931
#accession    C40905
#status       Preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues     133-411 ##label ESC
#superfamily  inhibin
#length       411 #molecular-weight 45182 #checksum 2167

CLASSIFICATION
SUMMARY

Query Match      51.4%; Score 471; DB 2; Length 411;
Best Local Similarity 48.3%; Pred. No.2,98e-88;
Matches          58; Conservative 27; Mismatches 34; Indels 1; Gaps 1;

Db      292 RIRKRGLECDGRTSLCCNQGFDFIRLIGMWDIITAPRGYGNCCESCPAYLAGVCGSA 351
      1 RARRTPTCEATPLCCRRDHYDFOEIOWGMDWIOEGYOLNCSQCCPHLAGSPGIA 60
      352 SSFRAAVNQGFRMGLNGPVSNCSCPTKLSMENVLFDDERYNVRKDPVMIVEEGCA 411
      61 ASFHAAYVSLKANNPWPAST-SCCVPARPRLPLLIDHNGNVKTDVDPDMVYEAACGS 119

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Search completed: Thu Aug 17 10:16:42 2000
Job time : 39 secs.

CC LENGTH: 119 amino acids
CC TYPE: amino acids
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: Internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;

Query Match 100.0%; Score 916; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
QY 1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
61 ASFSHSAVFSILKANNPWPASTSCCVPTARRPLSLILYLDHNGNVKTDVDMVVEACGCS 119
61 ASFSHSAVFSILKANNPWPASTSCCVPTARRPLSLILYLDHNGNVKTDVDMVVEACGCS 119

RESULT 2
ID US-09-184-933-12 STANDARD; PRT: 119 AA.
AC xxxxxx
DE

Sequence 12, Application US/09184933

CC GENERAL INFORMATION:
CC APPLICANT: Lee, Se-Jin
CC APPLICANT: Esquele, Aurora F.
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson, P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: US
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC OPERATING SYSTEM: Windows 95
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/184,933
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/274,215
CC FILING DATE: 13-JUL-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hallie, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07265/040001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-678-5070
CC TELEFAX: 619-68-5099

CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: Internal
SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;

Query Match 100.0%; Score 916; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
QY 1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
61 ASFSHSAVFSILKANNPWPASTSCCVPTARRPLSLILYLDHNGNVKTDVDMVVEACGCS 119
61 ASFSHSAVFSILKANNPWPASTSCCVPTARRPLSLILYLDHNGNVKTDVDMVVEACGCS 119

RESULT 3
ID US-08-274-215-12 STANDARD; PRT: 119 AA.
AC xxxxxx
DE

Sequence 12, Application US/08274215

CC GENERAL INFORMATION:
CC APPLICANT: Lee, Se-Jin
CC APPLICANT: Esquele, Aurora F.
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/274,215
CC FILING DATE: 13-JUL-1994
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hallie, Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07265/040001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212/765-5070
CC TELEFAX: 212/765-5070

CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: both
CC MOLECULE TYPE: protein
SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;

Query Match 100.0%; Score 916; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
QY 1 RARRPTCEPATPLCCGRDHYVDFQELGWRDWILOPEGYQLNYCGGCPHLAGSPGIA 60
61 ASFSHSAVFSILKANNPWPASTSCCVPTARRPLSLILYLDHNGNVKTDVDMVVEACGCS 119
61 ASFSHSAVFSILKANNPWPASTSCCVPTARRPLSLILYLDHNGNVKTDVDMVVEACGCS 119

RESULT 4
ID US-60-186-656-992 STANDARD: PRT: 131 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 992, Application US/60186656
XX
CC Sequence 992, Application US/60186656
CC GENERAL INFORMATION:
CC APPLICANT: Bonazzi, Vivien
CC TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
CC TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
CC FILE REFERENCE: CL000320
CC CURRENT APPLICATION NUMBER: US/60/186,656
CC CURRENT FILING DATE: 2000-03-03
CC NUMBER OF SEQ ID NOS: 1518
CC SOFTWARE: FastSeq for Windows Version 4.0
CC SEQ ID NO 992
CC LENGTH: 131
CC TYPE: PRT
CC ORGANISM: HUMAN
SQ SEQUENCE 131 AA: 14330 MW: 90159 CN;

Query Match 100.0%; Score 916; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 RARRRPTCEPATPLCCRDHYVDFOLGWRDIILOPEGYQLNYCSGCCPPLHAGSPGIA 72
QY 1 RARRRPTCEPATPLCCRDHYVDFOLGWRDIILOPEGYQLNYCSGCCPPLHAGSPGIA 60
QY 73 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 131
QY 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 5
ID US-60-185-361-608 STANDARD: PRT: 153 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 608, Application US/60185361
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CC Sequence 608, Application US/60185361
CC GENERAL INFORMATION:
CC APPLICANT: Bonazzi, Vivien
CC TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
CC TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
CC FILE REFERENCE: CL000291
CC CURRENT APPLICATION NUMBER: US/60/185,361
CC CURRENT FILING DATE: 2000-02-28
CC NUMBER OF SEQ ID NOS: 968
CC SOFTWARE: FastSeq for Windows Version 4.0
CC SEQ ID NO 608
CC LENGTH: 153
CC TYPE: PRT
CC ORGANISM: HUMAN
SQ SEQUENCE 153 AA: 16813 MW: 120970 CN;

Query Match 100.0%; Score 916; DB 3; Length 153;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 RARRRPTCEPATPLCCRDHYVDFOLGWRDIILOPEGYQLNYCSGCCPPLHAGSPGIA 94
QY 1 RARRRPTCEPATPLCCRDHYVDFOLGWRDIILOPEGYQLNYCSGCCPPLHAGSPGIA 60

Db 95 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 153
QY 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 6
ID US-60-212-356-257 STANDARD: PRT: 274 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 257, Application US/60212356
XX
CC Sequence 257, Application US/60212356
CC GENERAL INFORMATION:
CC APPLICANT: Beasley, Ellen
CC TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
CC TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
CC FILE REFERENCE: CL000677
CC CURRENT APPLICATION NUMBER: US/60/212,356
CC CURRENT FILING DATE: 2000-06-19
CC NUMBER OF SEQ ID NOS: 411
CC SOFTWARE: FastSeq for Windows Version 4.0
CC SEQ ID NO 257
CC LENGTH: 274
CC TYPE: PRT
CC ORGANISM: HUMAN
SQ SEQUENCE 274 AA: 29976 MW: 369765 CN;

Query Match 100.0%; Score 916; DB 23; Length 274;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 156 RARRRPTCEPATPLCCRDHYVDFOLGWRDIILOPEGYQLNYCSGCCPPLHAGSPGIA 215
QY 1 RARRRPTCEPATPLCCRDHYVDFOLGWRDIILOPEGYQLNYCSGCCPPLHAGSPGIA 60
QY 216 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 274
QY 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 7
ID US-09-521-978-4 STANDARD: PRT: 350 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 4, Application US/09521978
XX
CC Sequence 4, Application US/09521978
CC GENERAL INFORMATION:
CC APPLICANT: Ford, John E.
CC APPLICANT: Mize, Nancy K.
CC APPLICANT: Dickson, Mark C.
CC APPLICANT: Atterburn, Matthew C.
CC TITLE OF INVENTION: Methods And Materials Relating To Novel
CC TITLE OF INVENTION: Activin/Inhibin-Like Polypeptides
CC FILE REFERENCE: HYS-2
CC CURRENT APPLICATION NUMBER: US/09/521,978
CC CURRENT FILING DATE: 2000-03-09
CC NUMBER OF SEQ ID NOS: 4
CC SOFTWARE: PatentIn Ver. 2.1
CC SEQ ID NO 4
CC LENGTH: 350
CC TYPE: PRT
CC ORGANISM: Homo sapiens
SQ SEQUENCE 350 AA: 38561 MW: 616706 CN;

DT
XX
DE Sequence 13, Application US/08752919
CC
XX
CC General Information:
CC APPLICANT: Bonadio, Jeffrey
CC TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
CC TITLE OF INVENTION: OF LIVER ACTIVIN/INHIBIN AND METHODS BASED THEREON
CC NUMBER OF SEQUENCES: 72
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: NY
CC COUNTRY: USA
CC ZIP: 10036/2711
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/752,919
CC FILING DATE: 20-NOV-1996
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Coruzzi, Laura A
CC REGISTRATION NUMBER: 30,742
CC REFERENCE/DOCKET NUMBER: 8464-015
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212-790-9090
CC TELEFAX: 212-869-8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 251 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 251 AA; 28019 MW; 316319 CN;
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Best Local Similarity 97.5%; Pred. No. 9.23e-103;
Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 133 RARRRPTCEPPTPLCCRDHYVDFQELGMRDMLQPEGYQNTYCSGQCPHLAGSPGIA 192
DT
XX
AC xxxxxx
DT
XX
DE Sequence 4, Application US/08752919
CC
XX
CC General Information:
CC APPLICANT: Bonadio, Jeffrey
CC TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
CC TITLE OF INVENTION: OF LIVER ACTIVIN/INHIBIN AND METHODS BASED THEREON
CC NUMBER OF SEQUENCES: 72
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC

CC
CC CITY: New York
CC STATE: NY
CC COUNTRY: USA
CC ZIP: 10036/2711
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/752,919
CC FILING DATE: 20-NOV-1996
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Coruzzi, Laura A
CC REGISTRATION NUMBER: 30,742
CC REFERENCE/DOCKET NUMBER: 8464-015
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212-790-9090
CC TELEFAX: 212-869-8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 350 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 350 AA; 39057 MW; 619834 CN;
SO
Query Match 98.3%; Score 906; DB 13; Length 350;
Best Local Similarity 97.5%; Pred. No. 9.23e-103;
Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 232 RARRRPTCEPPTPLCCRDHYVDFQELGMRDMLQPEGYQNTYCSGQCPHLAGSPGIA 291
DT
XX
AC xxxxxx
DT
XX
DE Sequence 4023, Application US/60162247
CC
XX
CC General Information:
CC APPLICANT: Bonadio, Vivien
CC TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
CC TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AN
CC FILE REFERENCE: CLO00127
CC CURRENT APPLICATION NUMBER: US/60/162,247
CC CURRENT FILING DATE: 1999-10-29
CC NUMBER OF SEQ ID NOS: 9442
CC SOFTWARE: FASTSEQ for Windows Version 4.0
CC SEQ ID NO 4023
CC LENGTH: 112
CC TYPE: PRT
CC ORGANISM: Human
CC SEQUENCE 112 AA; 12324 MW; 66422 CN;
SO
Query Match 89.3%; Score 818; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.97e-91;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 8 PLCCRDHYVDFQELGMRDMLQPEGYQNTYCSGQCPHLAGSPGIAASFHSAVSLKA 67

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Page 7

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Job time : 191 secs.

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CC FRAGMENT TYPE: internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 119 AA: 13161 MW: 75307 CN:
Query Match 100.0%; Score 916; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,84e-81;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
QY 1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
61 ASFSHSAVSLKANNPWPASTSCVPTARRPPLSLYLIDHNGNVKTDVDPDVAEACGCS 119
QY 61 ASFSHSAVSLKANNPWPASTSCVPTARRPPLSLYLIDHNGNVKTDVDPDVAEACGCS 119
RESULT 2
ID US-08-765-662-12 STANDARD: PRT: 119 AA.
XX xxxxxx
AC

DE Sequence 12, Application US/08765662
CC Sequence 12, Application US/08765662
CC Patent No. 5929213
CC GENERAL INFORMATION:
CC APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/765.662
CC FILING DATE: 28-APR-1997
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08745
CC FILING DATE: 12-JUL-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halle, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-678-5070
CC TELEFAX: 619-678-5099
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acids
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 119 AA: 13161 MW: 75307 CN:
Query Match 100.0%; Score 916; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 2,84e-81;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
QY 1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
61 ASFSHSAVSLKANNPWPASTSCVPTARRPPLSLYLIDHNGNVKTDVDPDVAEACGCS 119
QY 61 ASFSHSAVSLKANNPWPASTSCVPTARRPPLSLYLIDHNGNVKTDVDPDVAEACGCS 119
RESULT 3
ID US-08-274-215A-12 STANDARD: PRT: 119 AA.
XX xxxxxx
AC
DE Sequence 12, Application US/08274215A
CC Patent No. 5831054
CC GENERAL INFORMATION:
CC APPLICANT: Lee, Se-Jin
CC APPLICANT: Esqueda, Aurora F.
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson, P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: US
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: Windows95
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/274.215A
CC FILING DATE: 13-JUL-1994
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halle, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07265/040001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-678-5070
CC TELEFAX: 619-66-5099
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
SQ SEQUENCE 119 AA: 13161 MW: 75307 CN:
Query Match 100.0%; Score 916; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,84e-81;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
QY 1 RARRPTPCPATPLCCRDHYVDFQELGWRDWILQPEGYOLNYCSGCCPPLHASPgia 60
61 ASFSHSAVSLKANNPWPASTSCVPTARRPPLSLYLIDHNGNVKTDVDPDVAEACGCS 119
QY 61 ASFSHSAVSLKANNPWPASTSCVPTARRPPLSLYLIDHNGNVKTDVDPDVAEACGCS 119

OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 4
PCT-US95-08745-14 STANDARD: PRT: 350 AA.
xxxxxx

Sequence 14, Application PC/TUS9508745

Sequence 14, Application PC/TUS9508745

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
City: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

SEQUENCE 350 AA: 38561 MW: 616706 CN:

Query Match 100.0%; Score 916; DB 4; Length 350;

Best Local Similarity 100.0%; Pred. No. 2,84e-81;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 233 RARRPTCEPATPLCCRDHYVDQELGMRDWILOPEGYOLNYCSCGCPPLASPGIA 291
OY 1 RARRPTCEPATPLCCRDHYVDQELGMRDWILOPEGYOLNYCSCGCPPLASPGIA 60
DB 292 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 350
OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 5
US-08-765-662-14 STANDARD: PRT: 350 AA.
xxxxxx

XX Sequence 14, Application US/08765662

XX Sequence 14, Application US/08765662

CC Patent No. 5929213
CC GENERAL INFORMATION:
CC APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 4225 Executive Square, Suite 1400
CC City: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,662

FILING DATE: 28-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08745

FILING DATE: 12-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Ph.D., Lisa A

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

SEQUENCE 350 AA: 38561 MW: 616706 CN:

Query Match 100.0%; Score 916; DB 2; Length 350;

Best Local Similarity 100.0%; Pred. No. 2,84e-81;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 232 RARRPTCEPATPLCCRDHYVDQELGMRDWILOPEGYOLNYCSCGCPPLASPGIA 291
OY 1 RARRPTCEPATPLCCRDHYVDQELGMRDWILOPEGYOLNYCSCGCPPLASPGIA 60
DB 292 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 350
OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 6
US-08-482-577B-4 STANDARD: PRT: 352 AA.
xxxxxx

Sequence 4, Application US/08482577B

Sequence 4, Application US/08482577B

Patent No. 5807713

Thu Aug 17 10:22:12 2000

US-08-765-662-12.ra1

Page 4

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CC GENERAL INFORMATION:  
CC APPLICANT : HOTTEN, GERTRUD  
CC APPLICANT : NEIDHARDT, HELGE  
CC APPLICANT : BECHTOLD, ROLF  
CC APPLICANT : POHL, JENS  
CC TITLE OF INVENTION : DNA SEQUENCES ENCODING NOVEL  
CC TITLE OF INVENTION : GROWTH/DIFFERENTIATION FACTORS  
CC NUMBER OF SEQUENCES : 49  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: NIVALDO, MARCELSTEIN, MURRAY, AND ORAM  
CC STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
CC CITY: WASHINGTON  
CC STATE: DC  
CC COUNTRY: USA  
CC ZIP: 20005  
CC COMPUTER READABLE FORM:  
CC MEDIA TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/482,577B  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: KLESNER, SHARON  
CC REGISTRATION NUMBER: 36,335  
CC REFERENCE/DOCKET NUMBER: P564-5010  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 202/638-5000  
CC TELEFAX: 202/638-4810  
CC INFORMATION FOR SEQ ID NO: 4:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 352 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC PUBLIC DOMAIN INFORMATION:  
CC DOCUMENT NUMBER: US 08/289,222  
CC FILING DATE: 12-AUG-1994  
CC SEQUENCE 352 AA; 39387 MW; 619423 CN;  
  
Query Match 68.7%; Score 629; DB 1; Length 352;  
Best Local Similarity 62.8%; Pred. No. 6,57e-52;  
Matches 76; Conservative 27; Mismatches 16; Indels 2; Gaps 2
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D3 RBRRRGIDCGGSGRMCCRQEFVDPDRRTGNWDWTIOEGYANNFCGGOPLHVAGMPGIS 291
I RRARRPTCEPNTPELCGRDHDHYDFQLGWMDWLTQEGYLNYCSCGCCPFILASFGIA 60

D4 ASHTAVLVLLKANAAGAATGTGSSCYSTRSRPSLIIYRDSDNIYKTDLPMWYEACGC 351
|||||:::|||||::: |||||::||| |:::||||| |
YY 61 ASHSASAFTSLKANNPW-PAS-TSCVPETARRPLSLILDHNNSNVKYTPDMWEAECGC 118

D5 352 S 352
YY 119 S 119

RESULT 7 STANDARD: PRt: 127 AA.
XX ID US-08-455-550-11
XX XXXXXX
DT XX
TX Sequence 11, Application US/08455550
DE Sequence 11, Application US/08455550
CX Patent No. 5670338
CG GENERAL INFORMATION:

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CC APPLICANT: MURAKAMI, KAZUO
CC APPLICANT: YENO, NAOTO
CC APPLICANT: KATO, YUKIO
CC TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Dike, Bronstein, Roberts & Cushman
CC STREET: 130 Water Street
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSO Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/98/455,550
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/056,564
CC FILING DATE: 30-APR-1993
CC APPLICATION NUMBER: 07/577,892
CC FILING DATE: 05-SEP-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Eisenstein, Ronald I
CC REGISTRATION NUMBER: 30628
CC REFERENCE/DOCKET NUMBER: 40302-FWC-DIV
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617-523-3400
CC TELEX: 617-523-6440
CC FAX: 200291
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 127 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHEetical: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC SEQUENCE 127 AA; 14256 MW; 78142 CN;

Query Match      67.4%; Score 617; DB 1; Length 127;
Best Local Similarity 62.2%; Pred. No. 1,09e+50;
Matches          74; Conservative   24; Mismatches 21; Indels    0; Gaps    0;

Db       9 HATKRLINDONSILCRKRDYVDPRDIDMNMWIKPBGQVINYCMGICPMHTAGAPGA 68
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy       1 RARRRPTEPARTPCCGRDIHYDFQLMRDMIIQPEGYOLNIGSGCPHLAGSPGIA 60
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       69 ASFTHTVLMLIKANNICTAVNSCCVPTRKRPLSMLYEDRNNNVLKTDIADMIYACGS 127
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy       61 ASPHSASVFSLKANNPWPASTISCVPTARRPISLLYLDHNNGNVKTDVDPDVMEACGS 119
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT      8
ID US-08-482-577B-2 STANDARD; PRT; 352 AA.
XX xxxxxx
XX
DT
DE Sequence 2, Application US/08482577B
CC Sequence 2, Application US/08482577B
CC Patent No. 5807713
CC GENERAL INFORMATION:
CC APPLICANT: HOTTEN, GERTRUD
CC
```


CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Wetherell, Jr. Ph.D., John R.
 CC REGISTRATION NUMBER: 31,678
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 19:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC IMMEDIATE SOURCE:
 CC CLONE: Inhibin betaA
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..121
 CC SEQUENCE 121 AA; 13757 MW; 76294 CN;
 SQ
 Query Match 54.4%; Score 498; DB 4; Length 121;
 Best Local Similarity 45.5%; Pred. No. 1,166-38;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 1 RRRRGLECDGKVNICKKQPFVSRFDIGWMDWIIAPSGYHANYCEGCPSHIAGTSSS 60
 1 RRRRTPTCEPATPLCCRDHYVDFQELGWRDWIIQPEGYQLNYCSGQCPHLAGSPGIA 60
 QY 61 LSFHSTVINHYRMGRHSPFANLKSCCVPFKLRPMSMLYYDDGQNIIRKDIQNMIVIECGC 120
 61 ASFHSAYFS-L-LKANNPWPASTSCCVPTARRPLSLIYLDHNGNVVKTDPDVMVYACGC 118
 Db 121 S 121
 QY 119 S 119
 RESULT 11
 ID PCT-US94-00666-21 STANDARD; PRT: 121 AA.
 XX
 AC xxxxxx
 DT
 XX
 XX
 DE Sequence 21, Application PC/TUS9400666
 CC Sequence 21, Application PC/TUS9400666
 CC GENERAL INFORMATION:
 CC APPLICANT: JOHNS HOPKINS UNIVERSITY
 CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
 CC NUMBER OF SEQUENCES: 29
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: SPENSLEY HORN JUBAS & LOBITZ
 CC STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 CC CITY: LOS ANGELES
 CC STATE: CALIFORNIA
 CC COUNTRY: US
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/00666
 CC FILING DATE: 12-JAN-1994
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: WETHERELL, JR. Ph.D., JOHN R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD2279 PCT

CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 21:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC IMMEDIATE SOURCE:
 CC CLONE: Inhibin beta A
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..121
 CC SEQUENCE 121 AA; 13757 MW; 76294 CN;
 SQ
 Query Match 54.4%; Score 498; DB 4; Length 121;
 Best Local Similarity 45.5%; Pred. No. 1,166-38;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 1 RRRRGLECDGKVNICKKQPFVSRFDIGWMDWIIAPSGYHANYCEGCPSHIAGTSSS 60
 1 RRRRTPTCEPATPLCCRDHYVDFQELGWRDWIIQPEGYQLNYCSGQCPHLAGSPGIA 60
 QY 61 LSFHSTVINHYRMGRHSPFANLKSCCVPFKLRPMSMLYYDDGQNIIRKDIQNMIVIECGC 120
 61 ASFHSAYFS-L-LKANNPWPASTSCCVPTARRPLSLIYLDHNGNVVKTDPDVMVYACGC 118
 Db 121 S 121
 QY 119 S 119
 RESULT 12
 ID US-08-481-377-21 STANDARD; PRT: 121 AA.
 XX
 AC xxxxxx
 DT
 XX
 XX
 DE Sequence 21, Application US/08481377
 CC Sequence 21, Application US/08481377
 CC Patent No. 5808007
 CC GENERAL INFORMATION:
 CC APPLICANT: JOHNS HOPKINS UNIVERSITY
 CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
 CC NUMBER OF SEQUENCES: 29
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: SPENSLEY HORN JUBAS & LOBITZ
 CC STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 CC CITY: LOS ANGELES
 CC STATE: CALIFORNIA
 CC COUNTRY: US
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/481,377
 CC FILING DATE: 514
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/00666
 CC FILING DATE: 12-JAN-1994
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: WETHERELL, JR. Ph.D., JOHN R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD2279 PCT
 CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 21:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC IMMEDIATE SOURCE:
 CC CLONE: Inhibin beta A
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..121
 CC SEQUENCE 121 AA: 13757 MW: 76294 CN:
 Query Match 54.4%; Score 498; DB 1; Length 121;
 Best Local Similarity 45.5%; Pred. No. 1,16e-38;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 1 RRRRLGECDEGKVICCKKQFVSEFKDIGNMDWIIAPSGYHANYCEGECPSHIAGTSGSS 60
 1 RRRRLPTCEPATPLCCRDHYDFQELGWRDWILOPEGYQNTYCSGQCPHLAGSPGIA 60
 Db 61 LSFHSTVINHYRMGRHSPFANLKSQCVPTKLRPMSMLYDDGQNIIRKDIQNMIVBECGC 120
 61 ASFSNAVFS-L-LKANNPWPASTSCCVPTARPLSLIYLDHNGNVVKTDPDMVVEACGC 118
 Db 121 S 121
 QY 119 S 119
 RESULT 13
 ID US-08-491-835-19 STANDARD; PRT: 121 AA.
 AC xxxxxx
 DE Sequence 19, Application US/08491835
 CC Sequence 19, Application US/08491835
 CC Patent No. 5821056
 CC GENERAL INFORMATION:
 CC APPLICANT: THE JOHNS HOPKINS UNIVERSITY
 CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
 CC NUMBER OF SEQUENCES: 26
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East, Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/491,835
 CC FILING DATE: 23-OCT-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/00685
 CC FILING DATE: 12-JAN-1994
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Welherell, Jr. Ph.D., John R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD3288
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100

CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 19:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC IMMEDIATE SOURCE:
 CC CLONE: Inhibin betaa
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..121
 CC SEQUENCE 121 AA: 13757 MW: 76294 CN:
 Query Match 54.4%; Score 498; DB 2; Length 121;
 Best Local Similarity 45.5%; Pred. No. 1,16e-38;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 1 RRRRLGECDEGKVICCKKQFVSEFKDIGNMDWIIAPSGYHANYCEGECPSHIAGTSGSS 60
 1 RRRRLPTCEPATPLCCRDHYDFQELGWRDWILOPEGYQNTYCSGQCPHLAGSPGIA 60
 Db 61 LSFHSTVINHYRMGRHSPFANLKSQCVPTKLRPMSMLYDDGQNIIRKDIQNMIVBECGC 120
 61 ASFSNAVFS-L-LKANNPWPASTSCCVPTARPLSLIYLDHNGNVVKTDPDMVVEACGC 118
 Db 121 S 121
 QY 119 S 119
 RESULT 14
 ID US-09-153-733A-21 STANDARD; PRT: 121 AA.
 AC xxxxxx
 DE Sequence 21, Application US/09153733A
 CC Sequence 21, Application US/09153733A
 CC Patent No. 6025475
 CC GENERAL INFORMATION:
 CC APPLICANT: JOHNS HOPKINS UNIVERSITY
 CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
 CC NUMBER OF SEQUENCES: 29
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
 CC STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 CC CITY: LOS ANGELES
 CC STATE: CALIFORNIA
 CC COUNTRY: US
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/09/153,733A
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 08/481,377
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: WETHERELL, JR. Ph.D., JOHN R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD2279 PCT
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110

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CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 121 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC IMMEDIATE SOURCE:
CC CLONE: Inhibin beta A
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..121
SQ SEQUENCE 121 AA; 13757 MW; 76294 CN;

Query Match 54.4%; Score 498; DB 3; Length 121;
Query Local Similarity 45.5%; Pred. No. 1,16e-38;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Dp 1 RRRRGLECDCKRVNICKCKQFFVSFKDIGNMDWIIAPSGYHANYCEGCPHSINGTSGSS 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 1 RARRRTPTICEARATPLCCGRDHYVDFQELGMDWIIQPEPGYIANTCSGCGPHLGGSGCIA 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
61 LSFHSTVYNHYRMGHSFFANLKKCCVFTKLRPMSMLYYDDGQNIIRKIDIONMIVEECGC 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
61 ASFSHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLIYLDHNGNVVKTDPDWMVVEACGC 118
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Dp 121 S 121
Qy 119 S 119

```

	CC	SEQUENCE CHARACTERISTICS:	INFO	ID NO:	23:
	CC	LENGTH:	122 amino acids		
	CC	TYPE:	amino acid		
	CC	STRANDEDNESS:	single		
	CC	TOPOLOGY:	linear		
	CC	MOLECULE TYPE:	protein		
	CC	IMMEDIATE SOURCE:			
	CC	CLONE:	Inhibin-beta-alpha		
	CC	FEATURE:			
	CC	NAME/KEY:	Protein		
	CC	LOCATION:	1..122		
	SQ	SEQUENCE	122 AA; 13894 MW; 77513 CN;		
Dd		Query Match	54.4% ; Score 498; DB 1; Length 122; Best Local Similarity 45.5%; Pred. No. 1,16e-38;		
OY		Matches	55; Conservative 32; Mismatches 32; Indels 2; Gaps 2.		
Dd	2	RRRRRLGGDGRVNICCKKFFVFSEFKIDGNMDITAPSCGYHAYCEGDEPSPIAGTSSS	61		
OY	1	RARRKRPTPEPATPLCCCRDRHYDFOELGWDMWILDPESGLNYCSGCCPPHLAASPGIA	60		
Dd	62	LSEFSTVINHHYMRGHSPFAMIKSCVPKLPRMSMLYYDDGONTIIRKDIONMTVEEGC	121		
OY	61	ASHSHAVFS-L-TKANPWPMPASTISCCVPTARRELSTLLTDHGNGVVKTIDVDPMVAECGC	118		
Dd	122 S 122				
OY	119 S 119				

Search completed: Thu Aug 17 10:20:29 2000
Job time : 34 secs.

XX Sequence 23, Application US/08455559
 CC
 CC Sequence 23, Application US/08455559
 CC Patent No. 5801014
 CC GENERAL INFORMATION:
 CC APPLICANT: LEE, SE-JIN
 CC APPLICANT: HUYNH, THANH
 CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
 CC NUMBER OF SEQUENCES: 27
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: SPENSLERY HORN JUBAS & LUBITZ
 CC STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 CC CITY: LOS ANGELES
 CC STATE: CALIFORNIA
 CC COUNTRY: US
 CC ZIP: 90067
 CC
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/455,559
 CC FILING DATE: 31-MAY-1995
 CC CLASSIFICATION: 435
 CC
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/003,144
 CC FILING DATE: 12-JAN-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: WETHERELL, JR. PH.D., JOHN R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: PD2280
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619/455-5100
 CC TELEFAX: 619-455-5110

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CC CC INFORMATION FOR SEQ ID NO: 23:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 122 amino acids
CC CC TYPE: amino acid
CC CC STRANDEDNESS: single
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC IMMEDIATE SOURCE:
CC CC CLONE: Inhibin-beta-alpha
CC CC FEATURE:
CC CC NAME/KEY: Protein
CC CC LOCATION: 1..122
SQ SQ SEQUENCE 122 AA; 13894 MW; 77513 CN;

Query Match 54.4%; Score 498; DB 1; Length 122;
Best Local Similarity 45.5%; Pred. No. 1,16e-38;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps

Db 2 RRRRRGLCEDGKRVNICCKQPFVSEFKDIGNNDWIIAPSGYHANYCEGECPSHIAGTSSS 61
QY 1 RARRRRPTCEPATPLCCRDHYVDFQELGWRDWIIQPEGYQLNYCSGCCPHIAGSPCIA 60
Db 62 LSFHSIVNHYRMKRGHSPFANLAKSCVPTKLRPMSMLYYDDGQNIKKDIONMIVEECGC 121
QY 61 ASFHSAVFS-L-LKANNPWPASTSCVPTARRPLSLIYLDHNGNVYKTDVDPDVVEACGC 118

Db 122 S 122
QY 119 S 119

Search completed: Thu Aug 17 10:20:29 2000
Job time : 34 secs.

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 三、
 四、
 五、
 六、

(W.T.)

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```

search_pp      protein - protein database search, using Smith-Waterman algorithm
run on:        Thu Aug 17 10:16:58 2000;      MasPar time 5.83 Seconds
              632.596 Million cell updates/sec
Tabular output not generated.

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Title: >US-08-765-662-12
Description: (1-119) from 5929213..pep
Perfect Score: 916
Sequence: 1 RARRRTPCTCEAIPFLCCRD.....NNNVYKTDVPMVYEAAGCS 119

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Scoring table: PAM 150
Gap 11

Searched: 85661 seqs, 30989116 residues

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Post-processing: Minimum Match 08
                  Listing first 45 summaries
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Database:      swiss-prot38
               1:swissprot
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Statistics: Mean 40.432; Variance 56.147; scale 0.720

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred. No.
1	905	98.9	350	1	INBE_MOUSE	INHIBIN BETA E CHAIN P	1.23e-229
2	899	98.1	350	1	INBE_RAT	INHIBIN BETA E CHAIN P	1.53e-227
3	632	67.0	352	1	INBC_MOUSE	INHIBIN BETA C CHAIN P	2.46e-148
4	616	67.2	352	1	INBC_HUMAN	INHIBIN BETA C CHAIN P	1.21e-143
5	506	55.9	426	1	INBA_HORSE	INHIBIN BETA A CHAIN P	1.12e-111
6	503	55.9	425	1	INBA_SHEEP	INHIBIN BETA A CHAIN P	9.00e-111
7	498	55.4	424	1	INBA_MOUSE	INHIBIN BETA A CHAIN P	2.49e-109
8	498	55.4	424	1	INBA_RAT	INHIBIN BETA A CHAIN P	2.49e-109
9	498	55.4	424	1	INBA_PIG	INHIBIN BETA A CHAIN P	2.49e-109
10	498	55.4	425	1	INBA_BOVIN	INHIBIN BETA A CHAIN P	2.49e-109
11	498	55.4	426	1	INBA_HUMAN	INHIBIN BETA A CHAIN P	2.49e-109
12	477	52.1	424	1	INBA_CHICK	INHIBIN BETA A CHAIN P	2.75e-103
13	474	51.7	391	1	INBB_CHICK	INHIBIN BETA B CHAIN P	2.00e-102
14	471	51.4	355	1	INBB_MOUSE	INHIBIN BETA B CHAIN P	1.45e-101
15	468	51.1	349	1	INBB_PIG	INHIBIN BETA B CHAIN P	1.05e-100
16	468	51.1	407	1	INBB_HUMAN	INHIBIN BETA B CHAIN P	1.05e-100
17	468	51.1	408	1	INBB_BOVIN	INHIBIN BETA B CHAIN P	1.05e-100
18	359	39.2	355	1	DVAL_BRARE	INH1N PROTEIN PRECURSO	7.68e-70
19	355	38.8	398	1	BMP4_XENLA	BONE MORPHOGENETIC PRO	1.00e-68
20	355	38.8	398	1	BMP4_XENLA	BONE MORPHOGENETIC PRO	1.00e-68
21	352	38.4	401	1	BMP4_XENLA	BONE MORPHOGENETIC PRO	6.84e-68
22	352	38.4	408	1	BMP4_MOUSE	BONE MORPHOGENETIC PRO	6.84e-68
23	352	38.4	408	1	BMP4_HUMAN	BONE MORPHOGENETIC PRO	6.84e-68

24	352	38.4	408	1	BMP4_DAMPA	BONE MORPHOGENETIC PRO	6.84e-68
25	352	38.4	408	1	BMP4_RAT	BONE MORPHOGENETIC PRO	6.84e-68
26	351	38.3	405	1	BMP4_CHICK	BONE MORPHOGENETIC PRO	1.30e-67
27	350	38.2	393	1	BMP2_RAT	BONE MORPHOGENETIC PRO	2.46e-67
28	350	38.2	394	1	BMP2_MOUSE	BONE MORPHOGENETIC PRO	2.46e-67
29	350	38.2	395	1	BMP2_RABBIT	BONE MORPHOGENETIC PRO	2.46e-67
30	350	38.2	396	1	BMP2_HUMAN	BONE MORPHOGENETIC PRO	2.46e-67
31	350	38.2	396	1	BMP2_DAMPA	BONE MORPHOGENETIC PRO	2.46e-67
32	350	38.2	409	1	BMP4_RABBIT	BONE MORPHOGENETIC PRO	3.18e-66
33	346	37.8	353	1	BMP2_CHICK	BONE MORPHOGENETIC PRO	7.75e-65
34	341	37.2	372	1	GDF1_HUMAN	EMBRYONIC GROWTH/DIFFE	1.47e-64
35	340	37.1	383	1	UNIV1_STRAIN	UNIV1 PRECURSOR	4.52e-62
36	331	36.1	360	1	DVR1_XENLA	DVR-1 PROTEIN PRECURSO	4.52e-62
37	331	36.1	513	1	BMP6_HUMAN	BONE MORPHOGENETIC PRO	4.52e-62
38	327	35.7	207	1	BMP6_RAT	BONE MORPHOGENETIC PRO	5.73e-61
39	327	35.7	510	1	BMP6_MOUSE	BONE MORPHOGENETIC PRO	5.73e-61
40	326	35.6	621	1	DECA4_DROPS	DECAPENTALEGIC PROTEI	1.08e-60
41	324	35.4	337	1	GDF1_MOUSE	EMBRYONIC GROWTH/DIFFE	3.84e-60
42	324	35.4	553	1	DECA4_DROST	DECAPENTALEGIC PROTEI	3.84e-60
43	323	35.3	588	1	DECA4_DROME	DECAPENTALEGIC PROTEI	7.24e-60
44	321	35.0	450	1	BMP7_MOUSE	BONE MORPHOGENETIC PRO	2.46e-59
45	320	34.9	451	1	BMP7_HUMAN	BONE MORPHOGENETIC PRO	4.83e-59

ALIGNMENTS

```

RESULT      1      STANDARD:      PRT:      350 AA.
ID          1      IHEB_MOUSE
AC          00871;
DT          15-JUL-1999 (Rel. 38, Created)
DT          15-JUL-1999 (Rel. 38, Last sequence update)
DT          15-JUL-1999 (Rel. 38, Last annotation update)
DE          INHIBIN BETA E CHAIN PRECURSOR (ACTIVIN BETA-E CHAIN).
GN          INHBE.
OS          Mus musculus (Mouse).
OC          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE=LIVER;
RC          MEDLINE; 97096313.
RA          Fang J., Yin W., Smiley E., Wang S.O., Bonadio J.;
RT          "Molecular cloning of the mouse activin beta E subunit gene.";
RL          Biochem. Biophys. Res. Commun. 228:669-674(1996).
RN          [2]
RP          MAPPING.
RX          MEDLINE; 97224404.
RA          Fang J., Wang S.O., Smiley E., Bonadio J.;
RT          "Gene coding for mouse activin beta C and beta E are closely linked
and exhibit a liver-specific expression pattern in adult tissues.";
RL          Biochem. Biophys. Res. Commun. 221:655-661(1997).
CC          -1- FUNCTION: INHIBINS ARE GONADAL GLYCOPROTEIDES THAT INHIBIT THE
CC          SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC          ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
CC          GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
CC          ECTODERMALIZATION, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
CC          CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
CC          DEVELOPMENT.
CC          -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC          -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC          -----
CC          This SWISS-PROT entry is copyright. It is produced through a collaboration
CC          between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC          the European Bioinformatics Institute. There are no restrictions on its
CC          use by non-profit institutions as long as its content is in no way
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CC          entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC          or send an email to license@isb-sib.ch).
CC          -----
DR          EMBL; U96386; AAB53801.1; -
DR          MGD; MGI109269; INHBE.
DR          PFM: PF00019; TGF-beta. 1.
DR          PRINTS; PR00438; GFCYSKNOT.

```

DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Follitropin Inhibitor; Contraceptive; Hormone; glycoprotein; signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 236 POTENTIAL.
 FT CHAIN 237 350 INHIBIN BETA E CHAIN.
 FT DISULFID 240 248 BY SIMILARITY.
 FT DISULFID 247 315 BY SIMILARITY.
 FT DISULFID 276 347 BY SIMILARITY.
 FT DISULFID 314 349 BY SIMILARITY.
 FT CARBOHYD 198 198 INTERCHAIN (BY SIMILARITY).
 SQ SEQUENCE 350 AA; 39057 MW; F37C76C8061D8AD9 CRC64;
 Query Match 98.9%; Score 906; DB 1; Length 350;
 Best Local Similarity 97.5%; Pred. No. 1,23e-229;
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 232 RARRPTCEPPTPLCCRRDHYVDFQELGWRDWILOPEGYQLNYCSGCCPPLHAGSPGIA 291
 1 RARRPTCEPPTPLCCRRDHYVDFQELGWRDWILOPEGYQLNYCSGCCPPLHAGSPGIA 60
 292 ASFSHSAVSLKANNPWPAGSCCVPFARPLSLYLIDHNGNVKTDVPMVVEACGCS 350
 61 ASFSHSAVSLKANNPWPASTSCVPFARPLSLYLIDHNGNVKTDVPMVVEACGCS 119

QY 61 ASFSHSAVSLKANNPWPASTSCVPFARPLSLYLIDHNGNVKTDVPMVVEACGCS 119

RESULT 2
 ID IHBC_RAT STANDARD; PRT: 350 AA.
 AC 088959;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INHIBIN BETA E CHAIN PRECURSOR (ACTIVIN BETA E CHAIN).
 GN INHBE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER, AND LUNG;
 RA O'Bryan M.K., Sebire K., Hedger M.P., Hearn M.T.W., de Kretser D.M.;
 RT "The cloning and regulation of the rat activin B subunit."
 RL Submitted (Sep-1998) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: INHIBINS ARE GONADAL GLYCOPROTEINS THAT INHIBIT THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 CC ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
 CC GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
 CC ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
 CC CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
 CC DEVELOPMENT.
 CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF089825; AAC36741.1; -
 DR PFAM: PF00019; TGF-beta.1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Follitropin Inhibitor; Contraceptive; Hormone; Glycoprotein; signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 236 POTENTIAL.
 FT CHAIN 237 350 INHIBIN BETA E CHAIN.
 FT DISULFID 240 248 BY SIMILARITY.
 FT DISULFID 247 315 BY SIMILARITY.
 FT DISULFID 276 347 BY SIMILARITY.

FT DISULFID 280 349 BY SIMILARITY.
 FT DISULFID 314 314 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 198 198 POTENTIAL.
 SQ SEQUENCE 350 AA; 38898 MW; 0CEBF6E108E926E3 CRC64;
 Query Match 98.1%; Score 899; DB 1; Length 350;
 Best Local Similarity 96.6%; Pred. No. 1.53e-227;
 Matches 115; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 232 RARRPTCEPPTPLCCRRDHYVDFQELGWRDWILOPEGYQLNYCSGCCPPLHAGSPGIA 291
 1 RARRPTCEPPTPLCCRRDHYVDFQELGWRDWILOPEGYQLNYCSGCCPPLHAGSPGIA 60
 292 ASFSHSAVSLKANNPWPAGSCCVPFARPLSLYLIDHNGNVKTDVPMVVEACGCS 350
 61 ASFSHSAVSLKANNPWPASTSCVPFARPLSLYLIDHNGNVKTDVPMVVEACGCS 119

QY 61 ASFSHSAVSLKANNPWPASTSCVPFARPLSLYLIDHNGNVKTDVPMVVEACGCS 119

RESULT 3
 ID IHBC_MOUSE STANDARD; PRT: 352 AA.
 AC P55104; 061452;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA C CHAIN).
 GN INHBC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129; TISSUE-LIVER;
 RC MEDLINE; 96435913.
 RA Schmitt J., Hoeltzen G., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Pohl J., Schrewe H.;
 RT "Structure, chromosomal localization, and expression analysis of the
 RT mouse inhibin/activin beta C (inhbc) gene."
 RL Genomics 32:358-366(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 96283807.
 RA Lau A.L., Nishimori K., Matzuk M.M.;
 RT "Structural analysis of the mouse activin beta C gene."
 RL Biochim. Biophys. Acta 1307:145-148(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 97224404.
 RA Fang J., Wang S.Q., Smalley E., Bonadio J.;
 RT "Genes coding for mouse activin beta C and beta E are closely linked
 RT and exhibit a liver-specific expression pattern in adult tissues."
 RL Biochem. Biophys. Res. Commun. 231:655-661(1997).
 CC -!- FUNCTION: INHIBINS ARE GONADAL GLYCOPROTEINS THAT INHIBIT THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 CC ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
 CC GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
 CC ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
 CC CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
 CC DEVELOPMENT.
 CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE ADULT LIVER.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC
 CC EMBL: X90841; CA662347.1; -
 DR EMBL: X90842; CA662347.1; JOINED.
 DR EMBL: X90819; CA62333.1; -

DR EMBL: U40773; AAC52723.1; -.
 DR EMBL: U40772; AAC52723.1; JOINED.
 DR EMBL: U95962; AAC53164.1; -.
 DR HSSP: P18075; 1BMP.
 DR MCD; MGI:105932; INHBC.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00672; INHIBINBC.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 KW FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 236
 FT CHAIN 237 352
 FT DISULFID 240 248
 FT DISULFID 247 317
 FT DISULFID 276 349
 FT DISULFID 280 351
 FT DISULFID 316 316
 FT CARBOHYD 111 111
 FT CARBOHYD 143 143
 FT CARBOHYD 161 161
 FT CARBOHYD 173 173
 FT CONFLICT 243 243
 FT SEQUENCE 352 AA; 39401 MW; 220812ED73717185 CRC64;
 SQ
 Query Match 69.0%; Score 632; DB 1; Length 352;
 Best Local Similarity 63.6%; Pred. No. 2,46e-148;
 Matches 77; Conservative 26; Mismatches 16; Indels 2; Gaps 2;
 Db 232 RVRRRGIDCGGSRMCCQOEFFVDFREIGMNDWIIOPGYAMNCTGCPPLHVGMGIS 291
 QY 1 RARRPTPCBPATPLCCRRDHYVDFELGMRDWIIQPGYGLNLCSGCPPLHVGSGEIA 60
 Db 292 ASFHRAVNLKANAAGATGGSCCVPTRRPLSLIYYDRDSNIVKTDIPDMVVEAGCG 351
 QY 61 ASFHRAVNSLKANNPW-PAS-TSCVPTARPLSLIYLDHNGNVKTDVDMVVEAGCG 118
 Db 352 S 352
 QY 119 S 119
 RESULT 4
 ID IHBC-HUMAN STANDARD; PRT; 352 AA.
 AC P55103;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 GN INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 95126961.
 RA Hoeten G., Weidhardt H., Schneider C., Pohl J.;
 RT "Cloning of a new member of the TGF-beta family: a putative new
 activin beta C chain."
 RL Biochem. Biophys. Res. Commun. 206:608-613(1995).
 CC -1- FUNCTION: INHIBINS ARE GONADAL GLYCOPROTEIDS THAT INHIBIT THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 CC ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
 CC GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
 CC ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
 CC CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
 CC DEVELOPMENT.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC or send an email to license@sib-sib.ch).
 DR EMBL: X82540; CAAS7890.1; -.
 DR HSSP: P18075; 1BMP.
 DR MIM: 601233; -.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00672; INHIBINBC.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 KW FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 236
 FT CHAIN 237 352
 FT DISULFID 240 248
 FT DISULFID 247 317
 FT DISULFID 276 349
 FT DISULFID 280 351
 FT DISULFID 316 316
 FT CARBOHYD 110 110
 FT CARBOHYD 143 143
 FT CARBOHYD 161 161
 FT SEQUENCE 352 AA; 38238 MW; 496476AD82562D3E CRC64;
 SQ
 Query Match 67.2%; Score 616; DB 1; Length 352;
 Best Local Similarity 63.9%; Pred. No. 1,21e-143;
 Matches 76; Conservative 26; Mismatches 15; Indels 2; Gaps 2;
 Db 234 HREGIDCGGSRMCCQOEFFVDFREIGMNDWIIOPGYAMNCTGCPPLHVGMGIS 293
 QY 3 RRRPTPCBPATPLCCRRDHYVDFELGMRDWIIQPGYGLNLCSGCPPLHVGSGEIA 62
 Db 294 FTHAVNLKANAAGATGGSCCVPTRRPLSLIYYDRDSNIVKTDIPDMVVEAGCG 352
 QY 63 FTHAVNSLKANNPW-PAS-TSCVPTARPLSLIYLDHNGNVKTDVDMVVEAGCG 119
 Db 352 S 352
 QY 426 S 426
 RESULT 5
 ID IHBA-HORSE STANDARD; PRT; 426 AA.
 AC P55102;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 GN INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RX MEDLINE: 96031670.
 RA Yoshida S., Yamamouchi K., Hasegawa T., Ikeda A., Suzuki M.,
 RA Chang K., Matsuyama S., Nishihara M., Takahashi M.;
 RT "Molecular cloning of cDNA for equine ovarian inhibin/activin beta A
 subunit."
 RL J. Vet. Med. Sci. 57:469-473(1995).
 CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEID THAT INHIBITS THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 CC ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
 CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A DIMER OF BETA-A.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL: D50326; BAA0862.1; -
DR HSSP: P18075; IBM.
DR PFAM: PF00019; TGF-beta: 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR FOLLITROPIN Inhibitor: Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 28
FT PROPEP 29 310
FT CHAIN 311 426
FT DISULFID 314 322 INHIBIN BETA A CHAIN.
FT DISULFID 321 391 BY SIMILARITY.
FT DISULFID 350 423 BY SIMILARITY.
FT DISULFID 354 425 BY SIMILARITY.
FT DISULFID 380 390 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 POTENTIAL.
SQ SEQUENCE 426 AA; 47709 MW; E481060B8368A77D CRC64;

Query Match 55.2%; Score 506; DB 1; Length 426;
Best Local Similarity 47.1%; Pred. No. 1,23e-11;
Matches 57; Conservative 30; Mismatches 32; Indels 2; Gaps 1;

DB 306 RRRRGLECDGKVNICKCKQFVSEFKDIGNMDMIAPSGYHANYCEGCEPSHIATSGSS 365
QY 1 RARRPTCEPATPLCCRDHYDFQELGMDMILOPEGYQLYNCGCOPHLAGSPGIA 60
DB 366 LSFHSTVINYRLRGHNPANLKSVCVPTKLPMMLYYDDGQNIKKIDIONMAYEECCG 425
QY 61 ASFHSAVFS-L-LKANMPASTSCCVPTARRPLSLIYLDHNGNVYKIDVPMVEACGC 118
DB 426 S 426
QY 119 S 119

RESULT 6
ID IHA-SHEEP STANDARD; PRT; 425 AA.
AC P43032;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95217464.
RA Fleming J.S., Galloway S.M., Crawford R.J., Tisdall D.J.,
RA Greenwood P.J.;
RT "Tissue-specific variation in the length of the 5' untranslated
RT region of the beta A-inhibin mRNA in sheep.";
RL Mol. Reprod. Dev. 40:1-8(1995).
CC -I- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -I- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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DR EMBL: L19218; AAC41621.1; -
DR HSSP: P18075; IBM.
DR PFAM: PF00019; TGF-beta: 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR FOLLITROPIN Inhibitor: Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 27
FT PROPEP 28 309
FT CHAIN 310 425
FT DISULFID 313 321 INHIBIN BETA A CHAIN.
FT DISULFID 320 390 BY SIMILARITY.
FT DISULFID 349 422 BY SIMILARITY.
FT DISULFID 353 424 BY SIMILARITY.
FT DISULFID 389 389 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 POTENTIAL.
SQ SEQUENCE 425 AA; 47565 MW; C910F7F64FF82F67 CRC64;

Query Match 54.9%; Score 503; DB 1; Length 425;
Best Local Similarity 46.3%; Pred. No. 9.00e-11;
Matches 56; Conservative 31; Mismatches 32; Indels 2; Gaps 2;

DB 305 RRRRGLECDGKVNICKCKQFVSEFKDIGNMDMIAPSGYHANYCEGCEPSHIATSGSS 364
QY 1 RARRPTCEPATPLCCRDHYDFQELGMDMILOPEGYQLYNCGCOPHLAGSPGIA 60
DB 365 LSFHSTVINYRLRGHNPANLKSVCVPTKLPMMLYYDDGQNIKKIDIONMAYEECCG 424
QY 61 ASFHSAVFS-L-LKANMPASTSCCVPTARRPLSLIYLDHNGNVYKIDVPMVEACGC 118
DB 425 S 425
QY 119 S 119

RESULT 7
ID IHA-MOUSE STANDARD; PRT; 424 AA.
AC Q04998;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93321614.
RA Albano P.M., Groome N., Smith J.C.;
RT "Activins are expressed in preimplantation mouse embryos and in ES
RT and EC cells and are regulated on their differentiation.";
RL Development 117:711-723(1993).
CC -I- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -I- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -I- TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC -----
 DR EMBL: X69619; CAA49325.1; -
 DR PIR: S31440; S31440.
 DR HSSP: P18075; 1BMP.
 DR MGD: MGI:96570; INHBA.
 DR PFAM: PF00688; TGF-beta; 1.
 DR PFAM: PF00438; GFCYKNOT.
 DR PRINTS: PR00670; INHIBINB.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1
 FT PROPEP 1
 FT CHAIN 1
 FT DISULFID 309 424 INHIBIN BETA A CHAIN.
 FT DISULFID 312 320 BY SIMILARITY.
 FT DISULFID 319 389 BY SIMILARITY.
 FT DISULFID 348 421 BY SIMILARITY.
 FT DISULFID 352 423 BY SIMILARITY.
 FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 165 165 POTENTIAL.
 FT SEQUENCE 424 AA; 47392 MW; 80C251B8754A7213 CRC64;
 SQ
 Query Match 54.4%; Score 498; DB 1; Length 424;
 Best Local Similarity 45.5%; Pred. No. 2,49e-109;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 304 RRRRGLECDGKVNICKCKOFVYFSDIGMNDWIIAPSGYHANYCEGCPSHIAGTSGSS 363
 1 RARRPTPCPEPATPLCCRDHYVDFQELGMRDWIIQPEGYQNTYCGSCCPPLAGSGIA 60
 Db 364 LSFHSTVINHYRMGHSFPANLKSQCVPTKLRPMSMLYDDGONIIKDIQNMIVBEGCG 423
 61 ASFSHSAVFS-L-LKANNPMPASTSCCVPTARRPLSLLYLDHNGNVVKTIDVPMVVEACGC 118
 Db 424 S 424
 QY 119 S 119
 RESULT 8
 ID INHBA-RAT STANDARD: PRT: 424 AA.
 AC P18331:
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 GN INHBA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91042598.
 RA Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;
 RT "Rat inhibin: molecular cloning of alpha- and beta-subunit
 RT complementary deoxyribonucleic acids and expression in the ovary.";
 RL Mol. Endocrinol. 1:561-568(1987).
 CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPOLYPEPTIDE THAT INHIBITS THE
 CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
 CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF BETA-A.
 CC ACTIVIN A IS A DIMER OF BETA-A.

 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: M37482; AAA41436.1; -
 DR PIR: B40056; B40056.
 DR HSSP: P18075; 1BMP.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PFAM: PF00688; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYKNOT.
 DR PROSITE: PS00250; INHIBINB.
 DR FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1
 FT PROPEP 1
 FT CHAIN 1
 FT DISULFID 309 424 INHIBIN BETA A CHAIN.
 FT DISULFID 312 320 BY SIMILARITY.
 FT DISULFID 319 389 BY SIMILARITY.
 FT DISULFID 348 421 BY SIMILARITY.
 FT DISULFID 352 423 BY SIMILARITY.
 FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 165 165 POTENTIAL.
 FT SEQUENCE 424 AA; 47406 MW; B2DAF7917FA50984 CRC64;
 SQ
 Query Match 54.4%; Score 498; DB 1; Length 424;
 Best Local Similarity 45.5%; Pred. No. 2,49e-109;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 304 RRRRGLECDGKVNICKCKOFVYFSDIGMNDWIIAPSGYHANYCEGCPSHIAGTSGSS 363
 1 RARRPTPCPEPATPLCCRDHYVDFQELGMRDWIIQPEGYQNTYCGSCCPPLAGSGIA 60
 Db 364 LSFHSTVINHYRMGHSFPANLKSQCVPTKLRPMSMLYDDGONIIKDIQNMIVBEGCG 423
 61 ASFSHSAVFS-L-LKANNPMPASTSCCVPTARRPLSLLYLDHNGNVVKTIDVPMVVEACGC 118
 Db 424 S 424
 QY 119 S 119
 RESULT 9
 ID INHBA-PIG STANDARD: PRT: 424 AA.
 AC P03970:
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 GN INHBA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX TISSUE-FOLLICULAR FLUID;
 RX MEDLINE: 86092207.
 RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
 RA Guillemin R., Niall H., Seeburg P.H.;
 RT "Complementary DNA sequences of ovarian follicular fluid inhibin show
 RT precursor structure and homology with transforming growth
 RT factor-beta.";
 RL Nature 318:659-663(1985).
 RN (2)
 RN SEQUENCE OF 309-323.
 RC TISSUE-FOLLICULAR FLUID;
 RX MEDLINE: 92355604.

RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
 RA Arikumi T., Yashiro T., Sugino K., Titani K., Sugino H.;
 RT "Isolation and characterization of native activin B.";
 RL J. Biol. Chem. 267:16385-16389(1992).
 CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
 CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
 CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A DIMER OF BETA-A.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: X03266; CAJ27020.1; -
 DR PIR: A01393; WFGGBA.
 DR HSSP: P18075; IBM.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PFAM: PF00688; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNT.
 DR PRINTS: PR00670; INHIBINBA.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 KW Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 308
 FT PROPEP 2 308
 FT CHAIN 309 424 INHIBIN BETA A CHAIN.
 FT DISULFID 312 320 BY SIMILARITY.
 FT DISULFID 319 389 BY SIMILARITY.
 FT DISULFID 348 421 BY SIMILARITY.
 FT DISULFID 352 423 BY SIMILARITY.
 FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 165 165 POTENTIAL.
 SQ SEQUENCE 424 AA; 47476 MW; 436BC6226FDAF52 CRC64;
 Query Match 54.4%; Score 498; DB 1; Length 424;
 Best Local Similarity 45.5%; Pred. No. 2,49e-109;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 304 RRRRGLECDKVNICKKPFVSKFDIGWMDWIAPSGYHANYCEGPCPSHIATSGSS 363
 1 RARRRTPTCEPATPLCCRDHYVDFELGWRDWILOPGYOLNCSGQCPHLAGSPeIA 60
 364 LSFHSTVINHYRMGHSFANLKSQCVPTKLRPSMMLYYDDGQNIKKDIONMIVECGC 423
 61 ASFSHSAVRS-L-LKANNWPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVEACGC 118
 Db 424 S 424
 QY 119 S 119
 RESULT 10
 ID IHBA_BOVIN STANDARD: PRT: 425 AA.
 AC P07995;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 GN INHBA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 95112839.
 RA Thompson D.A., Cronin C.N., Martin F.;
 RT "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
 RT and beta B-inhibin/activin genes. Identification of transcribed
 RT factor AP-2-binding sites in the 5'-flanking regions by DNase I
 RT footprinting.";
 RL Eur. J. Biochem. 226:751-764(1994).
 RN [2]
 RP SEQUENCE OF 258-425 FROM N.A.
 RC TISSUE=FOLLICULAR FLUID;
 RX MEDLINE: 86205842.
 RA Forage R.G., Ring J.M., Brown R.W., McInerney B.V., Cobon G.S.,
 RA Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
 RA Wettenhall R.E.H., Burger H.G., de Kretser D.M.;
 RT "Cloning and sequence analysis of cDNA species coding for the two
 RT subunits of inhibin from bovine follicular fluid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
 CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
 CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
 CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A DIMER OF BETA-A.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: U16239; AAB60627.1; -
 DR EMBL: U16238; AAB60627.1; JOINED.
 DR EMBL: M13274; AAA97415.1; -
 DR PIR: B25732; B25732.
 DR HSSP: P18075; IBM.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PFAM: PF00688; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNT.
 DR PRINTS: PR00670; INHIBINBA.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 KW Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein;
 FT SIGNAL 1 28
 FT PROPEP 29 309 BY SIMILARITY.
 FT CHAIN 310 425 INHIBIN BETA A CHAIN.
 FT DISULFID 313 321 BY SIMILARITY.
 FT DISULFID 313 390 BY SIMILARITY.
 FT DISULFID 320 349 BY SIMILARITY.
 FT DISULFID 349 422 BY SIMILARITY.
 FT DISULFID 353 424 BY SIMILARITY.
 FT DISULFID 389 389 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 165 165 POTENTIAL.
 SQ SEQUENCE 425 AA; 47521 MW; 2D8799D7197CDA37 CRC64;
 Query Match 54.4%; Score 498; DB 1; Length 425;
 Best Local Similarity 45.5%; Pred. No. 2,49e-109;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 305 RRRRGLECDKVNICKKPFVSKFDIGWMDWIAPSGYHANYCEGPCPSHIATSGSS 364
 1 RARRRTPTCEPATPLCCRDHYVDFELGWRDWILOPGYOLNCSGQCPHLAGSPeIA 60
 365 LSFHSTVINHYRMGHSFANLKSQCVPTKLRPSMMLYYDDGQNIKKDIONMIVECGC 424
 61 ASFSHSAVRS-L-LKANNWPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVEACGC 118
 QY 119 S 119

Db 425 S 425
OY 119 S 119

RESULT 11
ID ITHA_HUMAN STANDARD: PRT: 426 AA.
AC P08476; Q14599.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERTHROID DIFFERENTIATION PROTEIN) (EDF).
GN INHBA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
RX MEDLINE: 86186863.
RA Mason A.J., Miall H.D., Seeburg P.H.;
RT "Structure of two human ovarian inhibins.";
RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
[2]
RX MEDLINE: 88190086.
RA Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.;
RT "Erythroid differentiation factor is encoded by the same mRNA as that of the inhibin beta A chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).
[3]
RX MEDLINE: 92135888.
RA Tanimoto K., Handa S.I., Ueno N., Murekami K., Fukamizu A.;
RT "Structure and sequence analysis of the human activin beta A subunit gene.";
RL DNA Seq. 2:103-110(1991).
[4]
RX MEDLINE: 87005283.
RA Stewart A.G., Milborrow H.M., Ring J.M., Crowther C.E., Forage R.G.;
RL FEBS Lett. 206:329-334(1986).
[5]
RX MEDLINE: 311-426 FROM N.A.
RP TISSUE-TESTIS;
RT Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-A.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: M13436; AAA59168.1; -;
DR EMBL: X04447; CAA28041.1; -;
DR EMBL: X57578; CAA40805.1; -;
DR EMBL: X57579; CAA40805.1; JOINED.
DR EMBL: X57579; CAA40806.1; -;
DR EMBL: J03634; AAA35787.1; -;

DR EMBL: A14422; CAA01159.1; -;
DR EMBL: X72498; CAA51163.1; -;
DR PIR: A30884; A30884.
DR PIR: B24248; B24248.
DR PIR: B23556; B23556.
DR PIR: S30488; S30488.
DR HSSP: P18075; IBMP.
DR MIM: 147290; -;
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKOT.
DR PRINTS: PR00670; INHIBINB.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1
FT PROPEP 29 310
FT CHAIN 311 426
FT DISULFID 314 322
FT DISULFID 321 391
FT DISULFID 350 423
FT DISULFID 354 425
FT DISULFID 390 390
FT CARBOHYD 165 165
FT CONFLICT 377 379
SQ SEQUENCE 426 AA; 47442 MW; 201CDEDF9C8B6919 CRC64;
Query Match 54.4%; Score 498; DB 1; Length 426;
Best Local Similarity 45.5%; Pred. No. 2,49e-109;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
Db 306 RRRRGLECDGKVINCCCKQFFVSKFDIGNMDWIIASGHHANCEDECSHIAGTSGSS 365
OY 1 RARRPTCEPATPCPCCRDHYVDFQELGWRWILQEGVQLNCSQCCPHLAGSPGIA 60
Db 366 LSFHSTVINHYRMGSHSPFANLKCQVPTKLRPSMXYDDGNIIRKDIQNMIVBECGC 425
OY 61 ASFHSAVVS-L-KRANNWPASTSCCVPTARRPLSLYLIDHNGVAVTIDVDMVYEAACC 118
Db 426 S 426
OY 119 S 119

RESULT 12
ID ITHA_CHICK STANDARD: PRT: 424 AA.
AC P27092; Q90697;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=WHITE LEGHORN;
CC Huang J.X.;
CC Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=WHITE LEGHORN;
CC MEDLINE: 96380183.
CC Chen C.C., Johnson P.A.;
RT "Molecular cloning of inhibin/activin beta A-subunit complementary RT beta A-subunits in the domestic hen.";
RL Biol. Reprod. 54:429-435(1996).
[3]
RX MEDLINE: 317-349 FROM N.A.
RP TISSUE=HYPOBLAST;
RX MEDLINE: 91029482.

RA Mitran E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Brill A.;
RT "Activin can induce the formation of axial structures and is
RL expressed in the hypoblast of the chick."
Cell 63:495-501(1990).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: U26946; AAA68174.1; -;
DR EMBL: U42377; AAC59738.1; -;
DR EMBL: M61167; AAA48569.1; -;
DR EMBL: M57407; AAA03080.1; -;
DR PIR: B36193; B36193.
DR HSSP: P18075; IBM.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GRCYSKNOT.
DR PRINTS: PR00670; INHIBINB.
DR PROSITE: PS00250; TGF_BETA_1; FALSE NEG.
KW Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 28
FT PROPEP 29 308
FT CHAIN 309 424
FT DISULFID 312 320
FT DISULFID 319 389
FT DISULFID 348 421
FT DISULFID 352 423
FT DISULFID 388 388
FT CARBOHYD 165 165
FT CONFLICT 33 33
FT CONFLICT 87 87
FT CONFLICT 188 188
FT CONFLICT 213 213
FT CONFLICT 235 235
FT CONFLICT 307 307
FT CONFLICT 350 350
SQ SEQUENCE 424 AA; 47574 MW; 96E158FE119E1D69 CRC64;
Query Match 52.1%; Score 477; DB 1; Length 424;
Best Local Similarity 43.8%; Pred. No. 2.75e-103;
Matches 53; Conservative 32; Mismatches 34; Indels 2; Gaps 2;

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
CN INHIB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FOLLICLE.
RA Klingner H., Haleschek-Wiener J., Wohlrab B.K., Kuchler K., Wohlrab F.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-OVARY;
RA Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 311-381 FROM N.A.
RX MEDLINE; 91029482.
RA Mitran E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Brill A.;
RT "Activin can induce the formation of axial structures and is expressed
RL in the hypoblast of the chick."
Cell 63:495-501(1990).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: Z71594; CA96248.1; -;
DR EMBL: AF055478; AAC14187.1; -;
DR EMBL: M61166; AAA48568.1; -;
DR EMBL: M57408; AAA03079.1; -;
DR HSSP: P18075; IBM.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GRCYSKNOT.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 25
FT PROPEP 26 276
FT CHAIN 277 391
FT DISULFID 280 288
FT DISULFID 287 356
FT DISULFID 316 388
FT DISULFID 320 390
FT DISULFID 355 355
FT CARBOHYD 77 77
FT CONFLICT 30 30
SQ SEQUENCE 391 AA; 43608 MW; 060017BF33F7AF6C CRC64;
Query Match 51.7%; Score 474; DB 1; Length 391;
Best Local Similarity 49.2%; Pred. No. 2.00e-102;
Matches 59; Conservative 24; Mismatches 36; Indels 1; Gaps 1;

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Query Match          51.4% Score 471; DB 1; Length 255;
Best Local Similarity 48.3% Pred. No. 1,45e-101;
Matches            58; Conservative           27; Mismatches 34; Indels    1; Gaps    1;

Db      136 RIRKRGLECDGRTSLCCRQGFIDFRLIGWMDMIAPGTGYGNVCESGPYLAGVPSA 195
       1 1 1 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      1 RARRPTCEPFAFLPCCRDHYDFQELGRDMILQPEGYQLNCSGCCPHLGSPIA 60
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      196 SPSHAYAVNYOVRMGNGIPGVNSCCIPTLSMSMLTYEDDENIKRYRPMIYEBCGA 255
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      61 ASFSHAVFSLIKANNPMPAST -SCCPVARRPRLSLYIDHGNNVKTDVPMAVEACGS 119
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT   15
ID        INHB_PIG              STANDARD:             PRT:         349 AA.
AC        P04088;
DT        01-NOV-1986 (Rel. 03, Created)
DI        01-NOV-1986 (Rel. 03, Last sequence update)
DR        15-JUL-1998 (Rel. 36, Last annotation update)
DE        INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) (FRAGMENT).
GN        INHB.
OS        Sus scrofa (Pig).
OC        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC        Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN        [1]
RP        TISSUE-OVARIAN FOLLICULAR FLUID;
RC        MEDLINE; 86092207.
RX        Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
RA        Guillaume R., Niall H., Seeburg P.H.;
RT        "Complementary DNA sequences of ovarian follicular fluid inhibin show
RT        precursor structure and homology with transforming growth
RT        factor-beta."
RL        Nature 318:659-663(1985).
RN        [2]
RS        SEQUENCE OF 235-249.
RX        MEDLINE; 92355604.
RA        Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
RA        Atizumi T., Yasuiro T., Sugino K., Titani K., Sugino H.;
RT        "Isolation and characterization of native activin B.";
RJ        J.Biol.Chem. 267:16385-16389(1992).
CC        -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIDE THAT INHIBITS THE
CC        SECRETION OF FOLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC        ACTIVIN ACTIVATES THE SECRETION OF FOLITROPIN. ACTIVIN IS ALSO
CC        IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC        -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC        INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC        INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC        ACTIVIN AB IS A DIMER OF BETA-A.
CC        -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC        or send an email to license@isb-sib.ch).
CC
DB        EMBL, X03267; CAA27021.1; -.
DR        PIR; A01394; WPGGBB.
DR        HSSP; PI8075; IBMF.
DR        PFAM; PF00019; TGF-beta.1.
DR        Pfam; PF00688; TGFb_propeptide.1.
DR        PROSITE; PS00250; TGF_BETA.1.1.
KW        Folitropin inhibitor; Contrareceptive; Hormone; Glycoprotein.
FT        NON_TER
FT        1
FT        PROPEP
FT        <1
FT        CHAIN
FT        DISULFID
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 RELEASE
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Search: protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Aug 17 10:17:46 2000; MasPar time 13.47 Seconds
 612.688 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-662-12
 Description: (1-119) from 5929213.pep
 Perfect Score: 916
 Sequence: 1 RARRRTPCEPATPLCCRRD.....NGNVYKIDPDMVVEACGCS 119

Scoring table:
 PAM 150
 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: spiremb112
 1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
 5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
 9:sp.phage 10:sp.plant 11:sp.procent 12:sp.unclassified
 13:sp.vertibrate 14:sp.virus

Statistics: Mean 39.398; Variance 61.413; scale 0.642
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	630	68.8	351	11	09WUK5	8.97e-132
2	619	67.6	367	13	ACTIVIN BETA C.	6.80e-129
3	474	51.7	370	13	ACTIVIN D PRECURSOR.	2.67e-91
4	472	51.5	413	13	ACTIVIN BETA B SUBUNIT	8.69e-91
5	464	50.7	393	13	ACTIVIN BETA-A SUBUNIT	9.74e-89
6	439	47.9	138	13	ACTIVIN BETA B	2.36e-82
7	421	46.0	120	13	ACTIVIN BETA A PROTEIN	8.86e-78
8	415	45.3	119	13	ACTIVIN BETA B (FRAGMENT)	2.94e-76
9	397	43.3	104	13	ACTIVIN BETA-B SUBUNIT	1.04e-71
10	387	42.2	102	13	ACTIVIN BETA-A SUBUNIT	3.44e-69
11	386	42.1	102	13	ACTIVIN BETA-B-2 SUBUNIT	6.14e-69
12	385	42.0	102	13	ACTIVIN BETA-B-1 SUBUNIT	1.09e-68
13	382	41.7	361	5	BONE MORPHOGENETIC PRO	6.21e-68
14	362	39.5	365	5	DECAPENTAPLEGIC PROTEI	6.32e-63
15	362	39.5	365	5	CET-1.	6.32e-63
16	357	39.0	289	5	BONE MORPHOGENETIC PRO	1.12e-61
17	353	38.5	204	5	BONE MORPHOGENETIC PRO	1.11e-60
18	352	38.4	400	13	BONE MORPHOGENETIC PRO	1.96e-60
19	352	38.4	400	13	PROTEIN 4.	1.96e-60
20	352	38.4	400	13	BONE GENETIC PROTEIN 4	1.96e-60

Result ID	Score	Query Match	Length	ID	Description	Pred. No.
21	350	38.2	411	13	BMP2-4	6.18e-60
22	350	38.2	411	13	BONE MORPHOGENETIC PRO	6.18e-60
23	350	38.2	411	13	BONE MORPHOGENETIC PRO	6.18e-60
24	347	37.9	354	13	DERIERE.	3.44e-59
25	347	37.9	400	13	BMP4.	3.44e-59
26	344	37.6	386	13	BMP2.	1.91e-58
27	343	37.4	417	5	BONE MORPHOGENETIC PRO	3.38e-58
28	341	37.2	178	5	DECAPENTAPLEGIC (FRAG	1.06e-57
29	336	36.7	191	5	TRANSFORMING GROWTH FA	1.83e-56
30	334	36.5	301	5	MGDF PRECURSOR.	5.72e-56
31	333	36.4	373	13	GROWTH FACTOR CVG1.	1.01e-55
32	333	36.4	373	13	VGL1	1.01e-55
33	333	36.4	373	5	ACTIVIN BETA PRECURSOR	1.01e-55
34	333	36.4	428	5	TRANSFORMING GROWTH FA	1.01e-55
35	333	36.4	428	5	TRANSFORMING GROWTH FA	1.01e-55
36	337	35.7	443	5	HOMOLOG OF DPP SUBCLAS	3.06e-54
37	333	35.3	356	13	VGL1 PROTEIN (FRAGMENT)	2.96e-53
38	323	35.3	614	5	DECAPENTAPLEGIC PROTEI	2.96e-53
39	320	34.9	313	13	BONE MORPHOGENETIC PRO	1.62e-52
40	317	34.6	424	13	BONE MORPHOGENETIC PRO	8.84e-52
41	310	33.8	399	13	OSTEOGENIC DIFFERENTIA	4.60e-50
42	310	33.8	453	13	OSTEOGENIC DIFFERENTIA	4.60e-50
43	309	33.7	257	13	CONTRACT (FRAGMENT).	8.08e-50
44	309	33.7	261	13	GROWTH/DIFFERENTIATION	8.08e-50
45	308	33.6	126	13	PUTATIVE GROWTH/DIFFER	1.42e-49

ALIGNMENTS

Result ID	Score	Query Match	Length	ID	Description	Pred. No.
1	630	68.8	351	11	09WUK5	8.97e-132
2	619	67.6	367	13	ACTIVIN BETA C.	6.80e-129
3	474	51.7	370	13	ACTIVIN D PRECURSOR.	2.67e-91
4	472	51.5	413	13	ACTIVIN BETA B SUBUNIT	8.69e-91
5	464	50.7	393	13	ACTIVIN BETA-A SUBUNIT	9.74e-89
6	439	47.9	138	13	ACTIVIN BETA B	2.36e-82
7	421	46.0	120	13	ACTIVIN BETA A PROTEIN	8.86e-78
8	415	45.3	119	13	ACTIVIN BETA B (FRAGMENT)	2.94e-76
9	397	43.3	104	13	ACTIVIN BETA-B SUBUNIT	1.04e-71
10	387	42.2	102	13	ACTIVIN BETA-A SUBUNIT	3.44e-69
11	386	42.1	102	13	ACTIVIN BETA-B-2 SUBUNIT	6.14e-69
12	385	42.0	102	13	ACTIVIN BETA-B-1 SUBUNIT	1.09e-68
13	382	41.7	361	5	BONE MORPHOGENETIC PRO	6.21e-68
14	362	39.5	365	5	DECAPENTAPLEGIC PROTEI	6.32e-63
15	362	39.5	365	5	CET-1.	6.32e-63
16	357	39.0	289	5	BONE MORPHOGENETIC PRO	1.12e-61
17	353	38.5	204	5	BONE MORPHOGENETIC PRO	1.11e-60
18	352	38.4	400	13	BONE MORPHOGENETIC PRO	1.96e-60
19	352	38.4	400	13	PROTEIN 4.	1.96e-60
20	352	38.4	400	13	BONE GENETIC PROTEIN 4	1.96e-60

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DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE ACTIVIN D PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE: 95275314.
RA ODA S., NISHIMATSU S., MURAKAMI K., UENO N.;
RT "Molecular cloning and functional analysis of a new activin beta
RL subunit: a dorsal mesoderm-inducing activity in Xenopus.";
CC Biochem. Biophys. Res. Commun. 210:581-588(1995).
-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: D49543; BAA08494.1; -.
DR HSSP: P18075; 1BMP.
DR PROSITE: PS00250; TGF-BETA. 1.
DR PFAM: PF00019; TGF-beta. 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SIGNAL: Glycoprotein.
SQ SEQUENCE 367 AA; 41729 MW; E798693F CRC32;
  Query Match 67.6%; Score 619; DB 13; Length 367;
  Best Local Similarity 62.2%; Pred. No. 6,80e-129;
  Matches 74; Conservative 25; Mismatches 20; Indels 0; Gaps 0;

DB 249 HATKRSINDODNSLCCRDYVDKDGWMDWIKPEGYOINCMGLCPHMGAGPMA 308
  1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWIQLPBGYOLNCSGCPHLAGSPGIA 60
  61 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 119
  62 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 119

DB 309 ASFTHTVNLKANNIQTAVNSCCVPTKRRLPLMLFDRNNNVLTADIMIVACGCS 367
  1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWIQLPBGYOLNCSGCPHLAGSPGIA 60
  61 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 119

RESULT 3
ID 091350 PRELIMINARY; PRT; 370 AA.
AC 091350;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE ACTIVIN BETA B SUBUNIT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA DOHRMANN C.E., HEMMATTI-BRIVANLOU A., THOMSEN G.H., FIELDS A.,
RA WOLF T.M., MELTON D.A.;
RT "Expression of activin mRNA during early development in Xenopus
RL laevis.";
CC Dev. Biol. 157:474-483(1993).
-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: S61773; AAB26863.1; -.
DR HSSP: P18075; 1BMP.
DR PROSITE: PS00250; TGF-BETA. 1.
DR PFAM: PF00019; TGF-beta. 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SIGNAL: Glycoprotein.
SQ SEQUENCE 370 AA; 41678 MW; 58CE42C9 CRC32;
  Query Match 51.7%; Score 474; DB 13; Length 370;
  Best Local Similarity 48.3%; Pred. No. 2.67e-91;
  Matches 58; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

DB 251 RIRRGLECDHTNLCRCQGFYIDFRLGNWDWIAPAGYGNVCEGSPAVIAGVPSGA 310
  1 RIRRGLECDHTNLCRCQGFYIDFRLGNWDWIAPAGYGNVCEGSPAVIAGVPSGA 310
  1 RIRRGLECDHTNLCRCQGFYIDFRLGNWDWIAPAGYGNVCEGSPAVIAGVPSGA 310

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QY 1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWIQLPBGYOLNCSGCPHLAGSPGIA 60
DB 311 SSFTHTVNLKANNIQTAVNSCCVPTKRRLPLMLFDRNNNVLTADIMIVACGCS 370
  1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWIQLPBGYOLNCSGCPHLAGSPGIA 60
  61 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 119
  62 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 119

RESULT 4
ID 098660 PRELIMINARY; PRT; 413 AA.
AC 098660;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE ACTIVIN BETA-A SUBUNIT.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE: 96295508.
RA YAMAMOTO T., NAKAYAMA Y., ABE S.;
RT "Expression of activin beta subunit genes in Sertoli cells of newt
RL testes.";
CC Biochem. Biophys. Res. Commun. 224:451-456(1996).
-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: D84516; BAA12693.1; -.
DR HSSP: P18075; 1BMP.
DR PROSITE: PS00250; TGF-BETA. 1.
DR PFAM: PF00019; TGF-beta. 1.
DR PFAM: PF00688; TGF-beta. 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00670; INHIBINB.
DR SIGNAL: Glycoprotein.
SQ SEQUENCE 413 AA; 46303 MW; 77A4302D CRC32;
  Query Match 51.5%; Score 472; DB 13; Length 413;
  Best Local Similarity 43.0%; Pred. No. 8.69e-91;
  Matches 52; Conservative 33; Mismatches 34; Indels 2; Gaps 1;

DB 293 RRRKLECDGKVSIOCKQGFVSKFDIGWMDWYAPRGYANTYCEGCPMTITGSSG 352
  1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWIQLPBGYOLNCSGCPHLAGSPGIA 60
  61 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 118
  62 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 118

DB 353 PSFHAIVNQYMRGYSPTSVKSCVPTKLRMSMLYYDDGONIRKIDIONMVVEBCG 412
  61 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 118
  62 ASHSAVFSLLKANNPWPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVAVACGCS 118

DB 413 S 413
QY 119 S 119

RESULT 5
ID 090261 PRELIMINARY; PRT; 393 AA.
AC 090261;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE ACTIVIN BETA B.
GN ZACTBB OR ZACTBBTAA.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA WITTBRODT J., FREDERIC R.M.;
RT "Disruption of mesoderm and axis formation in fish by ectopic
RL expression of activin variants: the role of maternal activin.";
CC Genes Dev. 8:1448-1462(1994).
-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.

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DR EMBL: X76051; CAA53636.1; -.
DR HSSP: P18075; 1BMP.
DR ZFIN: ZDB-GENE-990415-2; zactbDb.
DR PROSITE: PS00250; TGF_BETA; 1.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR GLYCOPROTEIN.
KW SEQUENCE 393 AA; 43830 MW; 14DE189C CRC32;

Query Match
Best Local Similarity 47.9%; Score 464; DB 13; Length 393;
Matches 58; Conservative 24; Mismatches 37; Indels 2; Gaps 2;

Db 273 RIRKRGLEDGNNGLCCROQFYIDFRLIGNDWIIAPAGYIGNYCSCSPAYMAGVPGS 332
1 RARRRPTCEPATP-LCCRRDHYVDFOELGMRDWILOPEGYQNTNCSCGCPHLAGSPGI 59
333 ASSEFTAVVNOYRMGMSPGSMNSCIPTKLSTMSMLYFDEDEVNIYKRDYPMNIVEECG 392
60 AASFHSAVSLKANNPWPAST-SCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGC 118

Db 393 A 393
QY 119 S 119

RESULT 6
ID 09M6T9 PRELIMINARY: PRT: 138 AA.
AC 09M6T9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, last annotation update)
DE ACTIVIN BETA B PROTEIN (FRAGMENT).
GN ACTIVIN BETA B.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
KM SEQUENCE FROM N.A.
RA RODAWAY A., TAKEDA H., KOSHIDA S., PRICE B.M., SMITH J.C., PATIENT R.,
RA HOLDER N.;
RT Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
RT -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL: AJ238981; CAB43092.1; -.
DR PROSITE: PS00250; TGF_BETA; 1.
DR GLYCOPROTEIN.
KW NON_TER 1 1
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15263 MW; 9055EB6D CRC32;

Query Match
Best Local Similarity 49.1%; Score 439; DB 13; Length 138;
Matches 55; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

Db 21 CDGNGGLCCROQFYIDFRLIGNDWIIAPAGYIGNYCSCSPAYMAGVPGSASFTAV 80
1 RARRRPTCEPATP-LCCRRDHYVDFOELGMRDWILOPEGYQNTNCSCGCPHLAGSPGIASFHSAV 67
9 CBPAIP-LCCRRDHYVDFOELGMRDWILOPEGYQNTNCSCGCPHLAGSPGIASFHSAV 67

Db 81 VNOYRMGMSPGSMNSCIPTKLSTMSMLYFDEDEVNIYKRDYPMNIVEECG 132
68 FSLKANNPWPAST-SCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGC 118

RESULT 7
ID 09M6T8 PRELIMINARY: PRT: 120 AA.
AC 09M6T8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
DE ACTIVIN BETA A PROTEIN (FRAGMENT).

GN ACTIVIN BETA A.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
KM SEQUENCE FROM N.A.
RA RODAWAY A., TAKEDA H., KOSHIDA S., PRICE B.M., SMITH J.C., PATIENT R.,
RA HOLDER N.;
RT Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
RT -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL: AJ238980; CAB43091.1; -.
DR PROSITE: PS00250; TGF_BETA; 1.
DR GLYCOPROTEIN.
KW NON_TER 1 1
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13583 MW; B34108B8 CRC32;

Query Match
Best Local Similarity 46.0%; Score 421; DB 13; Length 120;
Matches 46; Conservative 34; Mismatches 29; Indels 2; Gaps 2;

Db 4 CDGARVCKRQFYIDFRLIGNDWIIAPAGYIGNYCSCSPAYMAGVPGS 63
9 CBPAIP-LCCRRDHYVDFOELGMRDWILOPEGYQNTNCSCGCPHLAGSPGIASFHSAV 68

Db 64 SHYRIGYSPFTNIKSCVPTARRPLSLYLIDHNGNVKTDVDMVVEACG 114
69 S-L-LKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACG 117

RESULT 8
ID 042125 PRELIMINARY: PRT: 119 AA.
AC 042125;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
DE ACTIVIN BETA B (FRAGMENT).
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Perciformes;
OC Perciformes; Percoidae; Sparidae; Chrysophrys.
RN [1]
KM SEQUENCE FROM N.A.
RA TISSUE-OVERY;
RA SAKAKIDA Y., KASAHARA M., INABA K.;
RT Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
RT -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL: AB006786; BAA22570.1; -.
DR HSSP: P18075; 1BMP.
DR PROSITE: PS00250; TGF_BETA; 1.
DR PFAM: PF00019; TGF-beta; 1.
DR GLYCOPROTEIN.
KW NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13455 MW; 3BBD4F6B CRC32;

Query Match
Best Local Similarity 45.3%; Score 415; DB 13; Length 119;
Matches 52; Conservative 24; Mismatches 33; Indels 1; Gaps 1;

Db 10 RIRKRGLEDGSSSLCCROQFYIDFRLIGNDWIIAPAGYIGNYCSCSPAYMAGVPGSA 69
1 RARRRPTCEPATP-LCCRRDHYVDFOELGMRDWILOPEGYQNTNCSCGCPHLAGSPGI 60

Db 70 SSFTAVVNOYRMGMSPGSMNSCIPTKLSTMSMLYFDEDEVNIYKRDY 119
61 AASFHSAVSLKANNPWPAST-SCCVPTARRPLSLYLIDHNGNVKTDV 109

RESULT 9
ID 098861 PRELIMINARY: PRT: 104 AA.

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AC 098861; 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DE 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE ACTIVIN BETA-B SUBUNIT (FRAGMENT).
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE; 96295508.
RA YAMAMOTO T., NAKAYAMA Y., ABE S.;
RT "Expression of activin beta subunit genes in seroli cells of newt
  testes."
RL Biochem. Biophys. Res. Commun. 224:451-456(1996).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; D84517; BAI12694.1; -.
DR HSSP; P18075; IBM.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DE Glycoprotein.
RN NON_TER 1
SQ SEQUENCE 104 AA; 11676 MW; 74527D82 CRC32;

Query Match 43.3%; Score 397; DB 13; Length 104;
Best Local Similarity 50.0%; Pred. No. 1,04e-71;
Matches 51; Conservative 21; Mismatches 29; Indels 1; Gaps 1.

DB 3 TNLCCROOFTIDFLRIGNDWIIITAPAGFGVNYCGSCPAIYAGPSGASSSHTTAVNQYR 62
QY 13 TPLCCRRHYVDFLGRMDWIIPEGYOLNVCSGGQCPHILAGSPGIAASHPSVFLSK 72
DB 63 MRGLPVTNNSCIPFTRKLTSMMLYFDEYNIYVRDYPNMIV 104
QY 73 ANNPWPAST-SCQVPTARPLSLITLDHNGNVVITDVPDMV 113

RESULT 10 PRELIMINARY; PRT; 102 AA.
AC 090390;
ID 090390;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE ACTIVIN BETA-A SUBUNIT (FRAGMENT).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinoidae; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE; 93290666.
RA GE W., GALLIN W.J., STROBECK C., PETER R.E.;
RT "Cloning and sequencing of goldfish activin subunit genes: strong
  structural conservation during vertebrate evolution."
RL Biochem. Biophys. Res. Commun. 193:711-717(1993).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; L15339; AAA49162.1; -.
DR HSSP; P18075; IBM.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DE Glycoprotein.
RN NON_TER 1
SQ SEQUENCE 102 AA; 11849 MW; 4B6A0E7C CRC32;

Query Match 42.2%; Score 387; DB 13; Length 102;
Best Local Similarity 43.4%; Pred. No. 3,44e-69;
Matches 43; Conservative 29; Mismatches 25; Indels 2; Gaps 2

4 VCKKQFVYVNRFDIGWSDMIITAPSGYHANYCEGDGCPSHVASITGSALSFHSYVINHYMR 63

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Oy		15	LCCRDHVVQDELGGWRMILOPBGYQLNVCSSGCCPHLASSPCILASFSFAVSFL-L-Tk	72
Dd		64	GYSPPNNIKSCCVPTRLRAMSMLTYNEOKRIKKDIONM	102
Oy		73	NNWPASTSCCVPTARRPLSLTLYLDHNNGNVKTDVPM	111
RESULT	11		PRELIMITARY;	PRT; 102 AA.
ID	090389			
AC	090389;			
DT	01-NOV-1996	(TREMBLrel_01,	Created)	
DR	01-NOV-1996	(TREMBLrel_01,	Last sequence update)	
DE	01-NOV-1999	(TREMBLrel_12,	Last annotation update)	
OS	ACTIVIN BETA-B-2 SUBUNIT	(FRAGMENT).		
OC	Carsassius auratus	(Goldfish).		
NC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;			
OC	Neoptelygili; Teleostei; Euteleostei; Ostariophysati; Cypriniformes;			
CC	Cyprinoidea; Cyprinidae; Cyprininae; Carsassius.	[1]		
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Blood:			
RC	MEDLINE: 93290666.			
RA	GE W., GALLIN W.J.. STROBECK C.; PETER R.E.;			
RT	"Cloning and sequencing of goldfish activin subunit genes: strong structural conservation during vertebrate evolution."			
Biochem. Biophys. Res. Commun.	193:711-717(1993)."			
-I-SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.				
EMBL: L15341; AAA49161.1; "				
HSSP: P18075; IAMP.				
PROSITE: PS00250; TGF_BETA; 1.				
PFAM: PF00019; TGF-beta; 1.				
Glycoprotein.				
NON_TER	1			
FT	NON_TER	1		
SQ	SEQUENCE	102 AA; 11342 MW; 89F12412 CRC32;		
Query Match		42.1%; Score 386; DB 13; Length 102;		
Best Local Similarity	51.0%;	Pred. No. 6.1e-63;		
Matches	50; Conservativity	19; Mismatches 28; Indels 1; Gaps 1.		
Dd		5	LCCRQOFIDRLTGWMDWIIPAGYYGNVCESGPCAFLAGPGSASSFHATVAAYNRMR	64
Oy		15	LCCRHDHVDPDLGGRDWIIOPBGTOLNYCSCGCCPHLASPCILASFSFAVSFLSKAN	74
Dd		65	GMSPSGVNSCCIPIKTLSMTLMFYDDENITRYKRYPNM	102
Oy		75	NFWPAST-SCCVPTARRPLSLTLYLDHNNGNVKTDVPM	111
RESULT	12		PRELIMITARY;	PRT; 102 AA.
ID	090388			
AC	090388;			
DT	01-NOV-1996	(TREMBLrel_01,	Created)	
DR	01-NOV-1996	(TREMBLrel_01,	Last sequence update)	
DE	01-NOV-1999	(TREMBLrel_12,	Last annotation update)	
OS	ACTIVIN BETA-B-1 SUBUNIT	(FRAGMENT).		
OC	Carsassius auratus	(Goldfish).		
NC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;			
OC	Neoptelygili; Teleostei; Euteleostei; Ostariophysati; Cypriniformes;			
CC	Cyprinoidea; Cyprinidae; Cyprininae; Carsassius.	[1]		
RN	SEQUENCE FROM N.A.			
RP	TISSUE=BLOOD:			
RC	MEDLINE: 93290666.			
RA	GE W., GALLIN W.J.. STROBECK C.; PETER R.E.;			
RT	"Cloning and sequencing of goldfish activin subunit genes: strong structural conservation during vertebrate evolution."			
Biochem. Biophys. Res. Commun.	193:711-717(1993)."			
-I-SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.				
EMBL: L15340; AAA49160.1; "				
HSSP: P10600; JKXK.				
PROSITE: PS00250; TGF_BETA; 1.				

DR PFAM: PF00019; TGF-beta; 1.
 KW Glycoprotein. 1
 FT NON_TER 102 102
 FT SEQUENCE 102 AA; 11358 MW; 6EFAB650 CRC32;
 Query Match 42.0%; Score 385; DB 13; Length 102;
 Best Local Similarity 50.0%; Pred. No. 1,09e-68;
 Matches 49; Conservative 20; Mismatches 28; Indels 1; Gaps 1;

Db 5 LCCROGFYDFRLIGNMWIIAPAGYGNCGSCPAYAGVGSASSFTAVVNOYRMR 64
 15 LCCRHHYVDFOLGKRDWILQPEGIQVNTCSGCPHLAGSGIAASHAVSFLKANN 74

Qy 65 GISPGSVNSCCIPPTKLTSMMLYFDEEYNVKKRVPNM 102
 75 NFWPAST-SCCVPTARRPRLSLYLIDHNGNVKTDVPM 111

RESULT 13
 ID 096504 PRELIMINARY; PRT; 361 AA.
 AC 096504;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE BONE MORPHOGENETIC PROTEIN 2/4.
 GN AMPRI BMP2/4.
 OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98401944.
 RA PANFOLIOU G.D., CLARK M.D., HOLLAND L.Z., LEHRACH H., HOLLAND N.D.;
 RT "Amphioxus bone morphogenetic protein closely related
 to Drosophila decapentaplegic and vertebrate BMP2 and BMP4: insights
 into evolution of dorsoventral axis specification.";
 RL dev. dyn. 213:130-139(1998).
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL: AF068750; AAC97486.1; -.
 DR HSSP: P18075; IBMF.
 DR PROSITE: PS00250; TGF-BETA; 1.
 KW Glycoprotein.
 SO SEQUENCE 361 AA; 41517 MW; 3C5F7B25 CRC32;

Query Match 41.7%; Score 382; DB 5; Length 361;
 Best Local Similarity 47.6%; Pred. No. 6,21e-68;
 Matches 49; Conservative 20; Mismatches 31; Indels 3; Gaps 3;

Db 260 CRRHSLYVDSVGNWDMVAPPGVQAYYCGECPFLAD-H-LNSTHAIYQTLVNSVN 317
 17 CRRDH-YVDFOLGKRDWILQPEGIQVNTCSGCPHLAGSGIAASHAVSFLKANN 75

Qy 318 PLAVKACCVPTDLSPISMYLNENDVYLVKNYODMVGCGC 360
 76 WWPASTSCCVPTARRPRLSLYLIDHNGNVKTDVPMVVEACGC 118

RESULT 14
 ID 002424 PRELIMINARY; PRT; 365 AA.
 AC 002424;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE DECAPENTAPLEGIC PROTEIN HOMOLOG.
 GN DEL-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N2.
 RA YANDELL M.D., ROSS R.M., SUZUKI Y., WOOD W.B.;

RT "Characteristics of dbi-1, a C. elegans decapentaplegic homologue,
 RT support a conserved role for BMP-family signaling in bilaterian
 RT development.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF004395; AAC27729.1; -.
 DR HSSP: P18075; IBMF.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 SO SEQUENCE 365 AA; 41768 MW; 7D3FDF49 CRC32;

Query Match 39.5%; Score 362; DB 5; Length 365;
 Best Local Similarity 41.2%; Pred. No. 6,32e-63;
 Matches 49; Conservative 28; Mismatches 37; Indels 5; Gaps 5;

Db 250 KGRKHNT-EAESNLCRTDFYVDFDLNMWDIMAPKGYD-AYOCGSCPPNMP-AQ-L 305
 1 KARRRPTCEPATPLCCRRHLYVDFOLGKRDWILQPEGIQVNTCSGCPHLAGSGI 59

Qy 306 NATNHAIQSLSLRPDEVPPCCVPTETSPISILYMDVYVIREYADMRVESCOC 364
 60 AASFHSAVFSLLKANNPWPASTSCCVPTARRPRLSLYLIDHNGNVKTDVPMVVEACGC 118

RESULT 15
 ID 076514 PRELIMINARY; PRT; 365 AA.
 AC 076514;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE CER-1.
 GN CER-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N2;
 RA MORITA K., CHOW K.L., UENO N.;
 RT "Body Length and Male Tail Ray Pattern Formation of C. elegans are
 RT Regulated by a Member of Tgfb Family";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF074395; AAC26791.1; -.
 DR HSSP: P18075; IBMF.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 SO SEQUENCE 365 AA; 41781 MW; 54051BBE CRC32;

Query Match 39.5%; Score 362; DB 5; Length 365;
 Best Local Similarity 41.2%; Pred. No. 6,32e-63;
 Matches 49; Conservative 28; Mismatches 37; Indels 5; Gaps 5;

Db 250 KGRKHNT-EAESNLCRTDFYVDFDLNMWDIMAPKGYD-AYOCGSCPPNMP-AQ-L 305
 1 KARRRPTCEPATPLCCRRHLYVDFOLGKRDWILQPEGIQVNTCSGCPHLAGSGI 59

Qy 306 NATNHAIQSLSLRPDEVPPCCVPTETSPISILYMDVYVIREYADMRVESCOC 364
 60 AASFHSAVFSLLKANNPWPASTSCCVPTARRPRLSLYLIDHNGNVKTDVPMVVEACGC 118

Search completed: Thu Aug 17 10:19:37 2000
 Job time : 111 secs.

